

- Location of Alignment in SEQ ID NO 404: from 138 to 155
- Alignment No. 4698
- gi No. 1150834
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 404: from 151 to 175
- Alignment No. 4699
- gi No. 119229
- % Identity 72.3
- Alignment Length 69
- Location of Alignment in SEQ ID NO 404: from 108 to 170
- Alignment No. 4700
- gi No. 120558
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 404: from 58 to 72
- Alignment No. 4701
- gi No. 121644
- % Identity 72.9
- Alignment Length 49
- Location of Alignment in SEQ ID NO 404: from 123 to 170
- Alignment No. 4702
- gi No. 1346180
- % Identity 72.1
- Alignment Length 64
- Location of Alignment in SEQ ID NO 404: from 108 to 168
- Alignment No. 4703
- gi No. 1346180
- % Identity 70.5
- Alignment Length 84
- Location of Alignment in SEQ ID NO 404: from 90 to 167
- Alignment No. 4704
- gi No. 1346181
- % Identity 70.4
- Alignment Length 85
- Location of Alignment in SEQ ID NO 404: from 90 to 166
- Alignment No. 4705
- gi No. 1346181
- % Identity 70.4
- Alignment Length 88
- Location of Alignment in SEQ ID NO 404: from 90 to 170
- Alignment No. 4706
- gi No. 1405559
- % Identity 70.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 404: from 76 to 162
- Alignment No. 4707
- gi No. 166374
- % Identity 71
- Alignment Length 31
- Location of Alignment in SEQ ID NO 404: from 142 to 172

- Alignment No. 4708
- gi No. 166374
- % Identity 71.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 404: from 130 to 175

- Alignment No. 4709
- gi No. 166376
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 404: from 56 to 69

- Alignment No. 4710
- gi No. 1938546
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 404: from 133 to 169

- Alignment No. 4711
- gi No. 2119044
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 404: from 131 to 170

- Alignment No. 4712
- gi No. 2119044
- % Identity 75.4
- Alignment Length 65
- Location of Alignment in SEQ ID NO 404: from 108 to 168

- Alignment No. 4713
- gi No. 2253105
- % Identity 72.2
- Alignment Length 54
- Location of Alignment in SEQ ID NO 404: from 102 to 155

- Alignment No. 4714
- gi No. 2253105
- % Identity 70.9
- Alignment Length 55
- Location of Alignment in SEQ ID NO 404: from 108 to 162

- Alignment No. 4715
- gi No. 2253105
- % Identity 70.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 404: from 114 to 170

- Alignment No. 4716
- gi No. 2267593
- % Identity 70.5
- Alignment Length 64
- Location of Alignment in SEQ ID NO 404: from 110 to 170

- Alignment No. 4717
- gi No. 2331133
- % Identity 70.5
- Alignment Length 64
- Location of Alignment in SEQ ID NO 404: from 110 to 170

- Alignment No. 4718
- gi No. 2388805
- % Identity 75.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 404: from 138 to 170

- Alignment No. 4719
- gi No. 2388805
- % Identity 73.5
- Alignment Length 35
- Location of Alignment in SEQ ID NO 404: from 110 to 143

- Alignment No. 4720
- gi No. 2388805
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 404: from 117 to 152

- Alignment No. 4721
- gi No. 2499130
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 404: from 131 to 148

- Alignment No. 4722
- gi No. 2499130
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 404: from 138 to 155

- Alignment No. 4723
- gi No. 2499130
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 404: from 139 to 156

- Alignment No. 4724
- gi No. 2499130
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 404: from 151 to 175

- Alignment No. 4725
- gi No. 2760483
- % Identity 70
- Alignment Length 41
- Location of Alignment in SEQ ID NO 404: from 120 to 159

- Alignment No. 4726
- gi No. 3183052
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 404: from 124 to 134

- Alignment No. 4727
- gi No. 322514
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 404: from 137 to 170

- Alignment No. 4728

- gi No. 322514
- % Identity 81.6
- Alignment Length 38
- Location of Alignment in SEQ ID NO 404: from 116 to 153

- Alignment No. 4729
- gi No. 322514
- % Identity 81.6
- Alignment Length 38
- Location of Alignment in SEQ ID NO 404: from 109 to 146

- Alignment No. 4730
- gi No. 322514
- % Identity 79.5
- Alignment Length 39
- Location of Alignment in SEQ ID NO 404: from 130 to 168

- Alignment No. 4731
- gi No. 322514
- % Identity 74.4
- Alignment Length 43
- Location of Alignment in SEQ ID NO 404: from 99 to 141

- Alignment No. 4732
- gi No. 322514
- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 404: from 91 to 134

- Alignment No. 4733
- gi No. 322702
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 404: from 56 to 76

- Alignment No. 4734
- gi No. 3875269
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 404: from 63 to 74

- Alignment No. 4735
- gi No. 3875269
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 404: from 90 to 103

- Alignment No. 4736
- gi No. 3875269
- % Identity 71.4
- Alignment Length 65
- Location of Alignment in SEQ ID NO 404: from 100 to 162

- Alignment No. 4737
- gi No. 3875441
- % Identity 72.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 404: from 142 to 170

- Alignment No. 4738
- gi No. 3881726

- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 404: from 59 to 72

- Alignment No. 4739
- gi No. 399783
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 404: from 132 to 168

- Alignment No. 4740
- gi No. 399783
- % Identity 73.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 404: from 111 to 148

- Alignment No. 4741
- gi No. 4455314
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 404: from 137 to 170

- Alignment No. 4742
- gi No. 4455314
- % Identity 81.6
- Alignment Length 38
- Location of Alignment in SEQ ID NO 404: from 116 to 153

- Alignment No. 4743
- gi No. 4455314
- % Identity 81.6
- Alignment Length 38
- Location of Alignment in SEQ ID NO 404: from 109 to 146

- Alignment No. 4744
- gi No. 4455314
- % Identity 79.5
- Alignment Length 39
- Location of Alignment in SEQ ID NO 404: from 130 to 168

- Alignment No. 4745
- gi No. 4455314
- % Identity 74.4
- Alignment Length 43
- Location of Alignment in SEQ ID NO 404: from 99 to 141

- Alignment No. 4746
- gi No. 4455314
- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 404: from 91 to 134

- Alignment No. 4747
- gi No. 4507911
- % Identity 70
- Alignment Length 41
- Location of Alignment in SEQ ID NO 404: from 120 to 159

- Alignment No. 4748
- gi No. 4581173
- % Identity 80.5

- Alignment Length 84
- Location of Alignment in SEQ ID NO 404: from 68 to 149

- Alignment No. 4749
- gi No. 4581173
- % Identity 77.5
- Alignment Length 94
- Location of Alignment in SEQ ID NO 404: from 93 to 181

- Alignment No. 4750
- gi No. 4581173
- % Identity 81.3
- Alignment Length 107
- Location of Alignment in SEQ ID NO 404: from 39 to 145

- Alignment No. 4751
- gi No. 4581173
- % Identity 71.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 404: from 73 to 181

- Alignment No. 4752
- gi No. 4581180
- % Identity 87.4
- Alignment Length 143
- Location of Alignment in SEQ ID NO 404: from 39 to 181

- Alignment No. 4753
- gi No. 544416
- % Identity 74.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 404: from 100 to 170

- Alignment No. 4754
- gi No. 544421
- % Identity 70.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 404: from 110 to 170

- Alignment No. 4755
- gi No. 544423
- % Identity 74.6
- Alignment Length 72
- Location of Alignment in SEQ ID NO 404: from 108 to 172

- Alignment No. 4756
- gi No. 544423
- % Identity 74
- Alignment Length 75
- Location of Alignment in SEQ ID NO 404: from 100 to 168

- Alignment No. 4757
- gi No. 544423
- % Identity 72.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 404: from 92 to 166

- Alignment No. 4758
- gi No. 544423
- % Identity 73.1
- Alignment Length 83

- Location of Alignment in SEQ ID NO 404: from 82 to 159
- Alignment No. 4759
- gi No. 5453938
- % Identity 70
- Alignment Length 41
- Location of Alignment in SEQ ID NO 404: from 131 to 170
- Alignment No. 4760
- gi No. 82087
- % Identity 70
- Alignment Length 62
- Location of Alignment in SEQ ID NO 404: from 108 to 167
- Alignment No. 4761
- gi No. 82696
- % Identity 70.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 404: from 113 to 170
- Alignment No. 4762
- gi No. 82696
- % Identity 73
- Alignment Length 65
- Location of Alignment in SEQ ID NO 404: from 108 to 170
- Alignment No. 4763
- gi No. 974605
- % Identity 70.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 404: from 66 to 147

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 405
- Ceres seq_id 1498401
- Location of start within SEQ ID NO 403: at 129 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4764
- Prion protein
- Location within SEQ ID NO 405: from 1 to 61 aa.
- Alignment No. 4765
- Prion protein
- Location within SEQ ID NO 405: from 11 to 107 aa.
- Alignment No. 4766
- Prion protein
- Location within SEQ ID NO 405: from 13 to 102 aa.
- Alignment No. 4767
- Prion protein
- Location within SEQ ID NO 405: from 20 to 113 aa.
- Alignment No. 4768
- Prion protein
- Location within SEQ ID NO 405: from 26 to 122 aa.
- Alignment No. 4769
- Prion protein

- Location within SEQ ID NO 405: from 36 to 136 aa.
- Alignment No. 4770
- Dehydrins
- Location within SEQ ID NO 405: from 1 to 104 aa.
- Alignment No. 4771
- Dehydrins
- Location within SEQ ID NO 405: from 13 to 138 aa.
- Alignment No. 4772
- Dehydrins
- Location within SEQ ID NO 405: from 25 to 138 aa.
- Alignment No. 4773
- Dehydrins
- Location within SEQ ID NO 405: from 39 to 123 aa.
- Alignment No. 4774
- Dehydrins
- Location within SEQ ID NO 405: from 39 to 138 aa.
- Alignment No. 4775
- Neurotransmitter-gated ion-channel
- Location within SEQ ID NO 405: from 5 to 62 aa.
- Alignment No. 4776
- Neurotransmitter-gated ion-channel
- Location within SEQ ID NO 405: from 89 to 139 aa.
- Alignment No. 4777
- 11-S plant seed storage protein
- Location within SEQ ID NO 405: from 1 to 128 aa.
- Alignment No. 4778
- 11-S plant seed storage protein
- Location within SEQ ID NO 405: from 1 to 132 aa.
- Alignment No. 4779
- 11-S plant seed storage protein
- Location within SEQ ID NO 405: from 7 to 138 aa.
- Alignment No. 4780
- 11-S plant seed storage protein
- Location within SEQ ID NO 405: from 11 to 123 aa.
- Alignment No. 4781
- 11-S plant seed storage protein
- Location within SEQ ID NO 405: from 11 to 128 aa.
- Alignment No. 4782
- 11-S plant seed storage protein
- Location within SEQ ID NO 405: from 11 to 138 aa.
- Alignment No. 4783
- 11-S plant seed storage protein
- Location within SEQ ID NO 405: from 12 to 120 aa.
- Alignment No. 4784
- 11-S plant seed storage protein
- Location within SEQ ID NO 405: from 12 to 137 aa.

- Alignment No. 4785
- 11-S plant seed storage protein
- Location within SEQ ID NO 405: from 14 to 138 aa.

- Alignment No. 4786
- 11-S plant seed storage protein
- Location within SEQ ID NO 405: from 15 to 120 aa.

- Alignment No. 4787
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 405: from 17 to 73 aa.

- Alignment No. 4788
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 405: from 23 to 80 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4789
- gi No. 1076731
- % Identity 73.4
- Alignment Length 82
- Location of Alignment in SEQ ID NO 405: from 48 to 126

- Alignment No. 4790
- gi No. 1076731
- % Identity 70.6
- Alignment Length 88
- Location of Alignment in SEQ ID NO 405: from 40 to 124

- Alignment No. 4791
- gi No. 1150834
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 405: from 89 to 106

- Alignment No. 4792
- gi No. 1150834
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 405: from 97 to 114

- Alignment No. 4793
- gi No. 1150834
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 405: from 96 to 113

- Alignment No. 4794
- gi No. 1150834
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 405: from 109 to 133

- Alignment No. 4795
- gi No. 119229
- % Identity 72.3
- Alignment Length 69
- Location of Alignment in SEQ ID NO 405: from 66 to 128

- Alignment No. 4796

- gi No. 120558
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 405: from 16 to 30

- Alignment No. 4797
- gi No. 121644
- % Identity 72.9
- Alignment Length 49
- Location of Alignment in SEQ ID NO 405: from 81 to 128

- Alignment No. 4798
- gi No. 1346180
- % Identity 72.1
- Alignment Length 64
- Location of Alignment in SEQ ID NO 405: from 66 to 126

- Alignment No. 4799
- gi No. 1346180
- % Identity 70.5
- Alignment Length 84
- Location of Alignment in SEQ ID NO 405: from 48 to 125

- Alignment No. 4800
- gi No. 1346181
- % Identity 70.4
- Alignment Length 85
- Location of Alignment in SEQ ID NO 405: from 48 to 124

- Alignment No. 4801
- gi No. 1346181
- % Identity 70.4
- Alignment Length 88
- Location of Alignment in SEQ ID NO 405: from 48 to 128

- Alignment No. 4802
- gi No. 1405559
- % Identity 70.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 405: from 34 to 120

- Alignment No. 4803
- gi No. 166374
- % Identity 71
- Alignment Length 31
- Location of Alignment in SEQ ID NO 405: from 100 to 130

- Alignment No. 4804
- gi No. 166374
- % Identity 71.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 405: from 88 to 133

- Alignment No. 4805
- gi No. 166376
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 405: from 14 to 27

- Alignment No. 4806
- gi No. 1938546

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- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 405: from 91 to 127

- Alignment No. 4807
- gi No. 2119044
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 405: from 89 to 128

- Alignment No. 4808
- gi No. 2119044
- % Identity 75.4
- Alignment Length 65
- Location of Alignment in SEQ ID NO 405: from 66 to 126

- Alignment No. 4809
- gi No. 2253105
- % Identity 72.2
- Alignment Length 54
- Location of Alignment in SEQ ID NO 405: from 60 to 113

- Alignment No. 4810
- gi No. 2253105
- % Identity 70.9
- Alignment Length 55
- Location of Alignment in SEQ ID NO 405: from 66 to 120

- Alignment No. 4811
- gi No. 2253105
- % Identity 70.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 405: from 72 to 128

- Alignment No. 4812
- gi No. 2267593
- % Identity 70.5
- Alignment Length 64
- Location of Alignment in SEQ ID NO 405: from 68 to 128

- Alignment No. 4813
- gi No. 2331133
- % Identity 70.5
- Alignment Length 64
- Location of Alignment in SEQ ID NO 405: from 68 to 128

- Alignment No. 4814
- gi No. 2388805
- % Identity 75.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 405: from 96 to 128

- Alignment No. 4815
- gi No. 2388805
- % Identity 73.5
- Alignment Length 35
- Location of Alignment in SEQ ID NO 405: from 68 to 101

- Alignment No. 4816
- gi No. 2388805
- % Identity 72.2

- Alignment Length 36
- Location of Alignment in SEQ ID NO 405: from 75 to 110

- Alignment No. 4817
- gi No. 2499130
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 405: from 89 to 106

- Alignment No. 4818
- gi No. 2499130
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 405: from 96 to 113

- Alignment No. 4819
- gi No. 2499130
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 405: from 97 to 114

- Alignment No. 4820
- gi No. 2499130
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 405: from 109 to 133

- Alignment No. 4821
- gi No. 2760483
- % Identity 70
- Alignment Length 41
- Location of Alignment in SEQ ID NO 405: from 78 to 117

- Alignment No. 4822
- gi No. 3183052
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 405: from 82 to 92

- Alignment No. 4823
- gi No. 322514
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 405: from 95 to 128

- Alignment No. 4824
- gi No. 322514
- % Identity 81.6
- Alignment Length 38
- Location of Alignment in SEQ ID NO 405: from 74 to 111

- Alignment No. 4825
- gi No. 322514
- % Identity 81.6
- Alignment Length 38
- Location of Alignment in SEQ ID NO 405: from 67 to 104

- Alignment No. 4826
- gi No. 322514
- % Identity 79.5
- Alignment Length 39

- Location of Alignment in SEQ ID NO 405: from 88 to 126
- Alignment No. 4827
- gi No. 322514
- % Identity 74.4
- Alignment Length 43
- Location of Alignment in SEQ ID NO 405: from 57 to 99
- Alignment No. 4828
- gi No. 322514
- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 405: from 49 to 92
- Alignment No. 4829
- gi No. 322702
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 405: from 14 to 34
- Alignment No. 4830
- gi No. 3875269
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 405: from 21 to 32
- Alignment No. 4831
- gi No. 3875269
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 405: from 48 to 61
- Alignment No. 4832
- gi No. 3875269
- % Identity 71.4
- Alignment Length 65
- Location of Alignment in SEQ ID NO 405: from 58 to 120
- Alignment No. 4833
- gi No. 3875441
- % Identity 72.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 405: from 100 to 128
- Alignment No. 4834
- gi No. 3881726
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 405: from 17 to 30
- Alignment No. 4835
- gi No. 399783
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 405: from 90 to 126
- Alignment No. 4836
- gi No. 399783
- % Identity 73.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 405: from 69 to 106

- Alignment No. 4837
- gi No. 4455314
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 405: from 95 to 128

- Alignment No. 4838
- gi No. 4455314
- % Identity 81.6
- Alignment Length 38
- Location of Alignment in SEQ ID NO 405: from 74 to 111

- Alignment No. 4839
- gi No. 4455314
- % Identity 81.6
- Alignment Length 38
- Location of Alignment in SEQ ID NO 405: from 67 to 104

- Alignment No. 4840
- gi No. 4455314
- % Identity 79.5
- Alignment Length 39
- Location of Alignment in SEQ ID NO 405: from 88 to 126

- Alignment No. 4841
- gi No. 4455314
- % Identity 74.4
- Alignment Length 43
- Location of Alignment in SEQ ID NO 405: from 57 to 99

- Alignment No. 4842
- gi No. 4455314
- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 405: from 49 to 92

- Alignment No. 4843
- gi No. 4507911
- % Identity 70
- Alignment Length 41
- Location of Alignment in SEQ ID NO 405: from 78 to 117

- Alignment No. 4844
- gi No. 4581173
- % Identity 80.5
- Alignment Length 84
- Location of Alignment in SEQ ID NO 405: from 26 to 107

- Alignment No. 4845
- gi No. 4581173
- % Identity 77.5
- Alignment Length 94
- Location of Alignment in SEQ ID NO 405: from 51 to 139

- Alignment No. 4846
- gi No. 4581173
- % Identity 81.3
- Alignment Length 107
- Location of Alignment in SEQ ID NO 405: from 1 to 103

- Alignment No. 4847
- gi No. 4581173
- % Identity 71.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 405: from 31 to 139

- Alignment No. 4848
- gi No. 4581180
- % Identity 87.4
- Alignment Length 143
- Location of Alignment in SEQ ID NO 405: from 1 to 139

- Alignment No. 4849
- gi No. 544416
- % Identity 74.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 405: from 58 to 128

- Alignment No. 4850
- gi No. 544421
- % Identity 70.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 405: from 68 to 128

- Alignment No. 4851
- gi No. 544423
- % Identity 74.6
- Alignment Length 72
- Location of Alignment in SEQ ID NO 405: from 66 to 130

- Alignment No. 4852
- gi No. 544423
- % Identity 74
- Alignment Length 75
- Location of Alignment in SEQ ID NO 405: from 58 to 126

- Alignment No. 4853
- gi No. 544423
- % Identity 72.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 405: from 50 to 124

- Alignment No. 4854
- gi No. 544423
- % Identity 73.1
- Alignment Length 83
- Location of Alignment in SEQ ID NO 405: from 40 to 117

- Alignment No. 4855
- gi No. 5453938
- % Identity 70
- Alignment Length 41
- Location of Alignment in SEQ ID NO 405: from 89 to 128

- Alignment No. 4856
- gi No. 82087
- % Identity 70
- Alignment Length 62
- Location of Alignment in SEQ ID NO 405: from 66 to 125

- Alignment No. 4857

- gi No. 82696
- % Identity 70.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 405: from 71 to 128

- Alignment No. 4858
- gi No. 82696
- % Identity 73
- Alignment Length 65
- Location of Alignment in SEQ ID NO 405: from 66 to 128

- Alignment No. 4859
- gi No. 974605
- % Identity 70.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 405: from 24 to 105

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 406
- Ceres seq_id 1498402
- Location of start within SEQ ID NO 403: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 111219

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 407
- Ceres seq_id 1498407

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 408
- Ceres seq_id 1498408
- Location of start within SEQ ID NO 407: at 153 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4860
- Fatty acid desaturase
- Location within SEQ ID NO 408: from 24 to 382 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4861
- gi No. 1054843
- % Identity 73.9
- Alignment Length 383
- Location of Alignment in SEQ ID NO 408: from 1 to 383

- Alignment No. 4862
- gi No. 1169598
- % Identity 99.7
- Alignment Length 383
- Location of Alignment in SEQ ID NO 408: from 1 to 383

- Alignment No. 4863
- gi No. 1345977
- % Identity 76
- Alignment Length 383
- Location of Alignment in SEQ ID NO 408: from 1 to 383

- Alignment No. 4864

- gi No. 2501790
- % Identity 74.9
- Alignment Length 384
- Location of Alignment in SEQ ID NO 408: from 1 to 383

- Alignment No. 4865
- gi No. 2564237
- % Identity 76.5
- Alignment Length 384
- Location of Alignment in SEQ ID NO 408: from 1 to 383

- Alignment No. 4866
- gi No. 2578033
- % Identity 71.4
- Alignment Length 385
- Location of Alignment in SEQ ID NO 408: from 1 to 382

- Alignment No. 4867
- gi No. 2613051
- % Identity 70.4
- Alignment Length 382
- Location of Alignment in SEQ ID NO 408: from 1 to 382

- Alignment No. 4868
- gi No. 3135020
- % Identity 74.2
- Alignment Length 383
- Location of Alignment in SEQ ID NO 408: from 1 to 383

- Alignment No. 4869
- gi No. 3264765
- % Identity 79
- Alignment Length 347
- Location of Alignment in SEQ ID NO 408: from 37 to 383

- Alignment No. 4870
- gi No. 3334184
- % Identity 90.1
- Alignment Length 384
- Location of Alignment in SEQ ID NO 408: from 1 to 383

- Alignment No. 4871
- gi No. 3417601
- % Identity 77.5
- Alignment Length 384
- Location of Alignment in SEQ ID NO 408: from 1 to 383

- Alignment No. 4872
- gi No. 3452129
- % Identity 84.6
- Alignment Length 384
- Location of Alignment in SEQ ID NO 408: from 1 to 383

- Alignment No. 4873
- gi No. 3452132
- % Identity 82.9
- Alignment Length 181
- Location of Alignment in SEQ ID NO 408: from 139 to 319

- Alignment No. 4874
- gi No. 3452135

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- % Identity 92.5
- Alignment Length 161
- Location of Alignment in SEQ ID NO 408: from 139 to 299

- Alignment No. 4875
- gi No. 4092879
- % Identity 91.3
- Alignment Length 312
- Location of Alignment in SEQ ID NO 408: from 57 to 367

- Alignment No. 4876
- gi No. 4378875
- % Identity 90.9
- Alignment Length 384
- Location of Alignment in SEQ ID NO 408: from 1 to 383

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 409
- Ceres seq_id 1498409
- Location of start within SEQ ID NO 407: at 171 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4877
- Fatty acid desaturase
- Location within SEQ ID NO 409: from 18 to 376 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4878
- gi No. 1054843
- % Identity 73.9
- Alignment Length 383
- Location of Alignment in SEQ ID NO 409: from 1 to 377

- Alignment No. 4879
- gi No. 1169598
- % Identity 99.7
- Alignment Length 383
- Location of Alignment in SEQ ID NO 409: from 1 to 377

- Alignment No. 4880
- gi No. 1345977
- % Identity 76
- Alignment Length 383
- Location of Alignment in SEQ ID NO 409: from 1 to 377

- Alignment No. 4881
- gi No. 2501790
- % Identity 74.9
- Alignment Length 384
- Location of Alignment in SEQ ID NO 409: from 1 to 377

- Alignment No. 4882
- gi No. 2564237
- % Identity 76.5
- Alignment Length 384
- Location of Alignment in SEQ ID NO 409: from 1 to 377

- Alignment No. 4883
- gi No. 2578033
- % Identity 71.4

- Alignment Length 385
- Location of Alignment in SEQ ID NO 409: from 1 to 376

- Alignment No. 4884
- gi No. 2613051
- % Identity 70.4
- Alignment Length 382
- Location of Alignment in SEQ ID NO 409: from 1 to 376

- Alignment No. 4885
- gi No. 3135020
- % Identity 74.2
- Alignment Length 383
- Location of Alignment in SEQ ID NO 409: from 1 to 377

- Alignment No. 4886
- gi No. 3264765
- % Identity 79
- Alignment Length 347
- Location of Alignment in SEQ ID NO 409: from 31 to 377

- Alignment No. 4887
- gi No. 3334184
- % Identity 90.1
- Alignment Length 384
- Location of Alignment in SEQ ID NO 409: from 1 to 377

- Alignment No. 4888
- gi No. 3417601
- % Identity 77.5
- Alignment Length 384
- Location of Alignment in SEQ ID NO 409: from 1 to 377

- Alignment No. 4889
- gi No. 3452129
- % Identity 84.6
- Alignment Length 384
- Location of Alignment in SEQ ID NO 409: from 1 to 377

- Alignment No. 4890
- gi No. 3452132
- % Identity 82.9
- Alignment Length 181
- Location of Alignment in SEQ ID NO 409: from 133 to 313

- Alignment No. 4891
- gi No. 3452135
- % Identity 92.5
- Alignment Length 161
- Location of Alignment in SEQ ID NO 409: from 133 to 293

- Alignment No. 4892
- gi No. 4092879
- % Identity 91.3
- Alignment Length 312
- Location of Alignment in SEQ ID NO 409: from 51 to 361

- Alignment No. 4893
- gi No. 4378875
- % Identity 90.9
- Alignment Length 384

- Location of Alignment in SEQ ID NO 409: from 1 to 377

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 410
- Ceres seq_id 1498410
- Location of start within SEQ ID NO 407: at 690 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4894
- Fatty acid desaturase
- Location within SEQ ID NO 410: from 1 to 203 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4895
- gi No. 1054843
- % Identity 73.9
- Alignment Length 383
- Location of Alignment in SEQ ID NO 410: from 1 to 204
- Alignment No. 4896
- gi No. 1169598
- % Identity 99.7
- Alignment Length 383
- Location of Alignment in SEQ ID NO 410: from 1 to 204
- Alignment No. 4897
- gi No. 1345977
- % Identity 76
- Alignment Length 383
- Location of Alignment in SEQ ID NO 410: from 1 to 204
- Alignment No. 4898
- gi No. 2501790
- % Identity 74.9
- Alignment Length 384
- Location of Alignment in SEQ ID NO 410: from 1 to 204
- Alignment No. 4899
- gi No. 2564237
- % Identity 76.5
- Alignment Length 384
- Location of Alignment in SEQ ID NO 410: from 1 to 204
- Alignment No. 4900
- gi No. 2578033
- % Identity 71.4
- Alignment Length 385
- Location of Alignment in SEQ ID NO 410: from 1 to 203
- Alignment No. 4901
- gi No. 2613051
- % Identity 70.4
- Alignment Length 382
- Location of Alignment in SEQ ID NO 410: from 1 to 203
- Alignment No. 4902
- gi No. 3135020
- % Identity 74.2
- Alignment Length 383
- Location of Alignment in SEQ ID NO 410: from 1 to 204

- Alignment No. 4903
- gi No. 3264765
- % Identity 79
- Alignment Length 347
- Location of Alignment in SEQ ID NO 410: from 1 to 204

- Alignment No. 4904
- gi No. 3334184
- % Identity 90.1
- Alignment Length 384
- Location of Alignment in SEQ ID NO 410: from 1 to 204

- Alignment No. 4905
- gi No. 3417601
- % Identity 77.5
- Alignment Length 384
- Location of Alignment in SEQ ID NO 410: from 1 to 204

- Alignment No. 4906
- gi No. 3452129
- % Identity 84.6
- Alignment Length 384
- Location of Alignment in SEQ ID NO 410: from 1 to 204

- Alignment No. 4907
- gi No. 3452132
- % Identity 82.9
- Alignment Length 181
- Location of Alignment in SEQ ID NO 410: from 1 to 140

- Alignment No. 4908
- gi No. 3452135
- % Identity 92.5
- Alignment Length 161
- Location of Alignment in SEQ ID NO 410: from 1 to 120

- Alignment No. 4909
- gi No. 4092879
- % Identity 91.3
- Alignment Length 312
- Location of Alignment in SEQ ID NO 410: from 1 to 188

- Alignment No. 4910
- gi No. 4378875
- % Identity 90.9
- Alignment Length 384
- Location of Alignment in SEQ ID NO 410: from 1 to 204

Maximum Length Sequence corresponding to clone ID 111254

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 411
- Ceres seq_id 1498411

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 412
- Ceres seq_id 1498412
- Location of start within SEQ ID NO 411: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4911

- Pectinesterase
- Location within SEQ ID NO 412: from 196 to 513 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4912
- gi No. 2529672
- % Identity 100
- Alignment Length 41
- Location of Alignment in SEQ ID NO 412: from 1 to 41
- Alignment No. 4913
- gi No. 2529672
- % Identity 96.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 412: from 67 to 168
- Alignment No. 4914
- gi No. 2529672
- % Identity 99.7
- Alignment Length 320
- Location of Alignment in SEQ ID NO 412: from 210 to 529
- Alignment No. 4915
- gi No. 2895514
- % Identity 78.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 412: from 363 to 440

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 413
- Ceres seq_id 1498413
- Location of start within SEQ ID NO 411: at 275 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4916
- Pectinesterase
- Location within SEQ ID NO 413: from 148 to 465 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4917
- gi No. 2529672
- % Identity 96.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 413: from 19 to 120
- Alignment No. 4918
- gi No. 2529672
- % Identity 99.7
- Alignment Length 320
- Location of Alignment in SEQ ID NO 413: from 162 to 481
- Alignment No. 4919
- gi No. 2895514
- % Identity 78.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 413: from 315 to 392

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 414
- Ceres seq_id 1498414

- Location of start within SEQ ID NO 411: at 368 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4920
- Pectinesterase
- Location within SEQ ID NO 414: from 117 to 434 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4921
- gi No. 2529672
- % Identity 96.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 414: from 1 to 89
- Alignment No. 4922
- gi No. 2529672
- % Identity 99.7
- Alignment Length 320
- Location of Alignment in SEQ ID NO 414: from 131 to 450
- Alignment No. 4923
- gi No. 2895514
- % Identity 78.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 414: from 284 to 361

Maximum Length Sequence corresponding to clone ID 112350

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 415
- Ceres seq_id 1498423

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 416
- Ceres seq_id 1498424
- Location of start within SEQ ID NO 415: at 235 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4924
- Mov34 family
- Location within SEQ ID NO 416: from 407 to 472 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 417
- Ceres seq_id 1498425
- Location of start within SEQ ID NO 415: at 394 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4925
- Mov34 family
- Location within SEQ ID NO 417: from 354 to 419 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 418
- Ceres seq_id 1498426
- Location of start within SEQ ID NO 415: at 487 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4926
- Mov34 family
- Location within SEQ ID NO 418: from 323 to 388 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 112720

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 419
- Ceres seq_id 1498427

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 420
- Ceres seq_id 1498428
- Location of start within SEQ ID NO 419: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 4927
- gi No. 2982456
- % Identity 100
- Alignment Length 371
- Location of Alignment in SEQ ID NO 420: from 16 to 386

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 421
- Ceres seq_id 1498429
- Location of start within SEQ ID NO 419: at 47 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 4928
- gi No. 2982456
- % Identity 100
- Alignment Length 371
- Location of Alignment in SEQ ID NO 421: from 1 to 371

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 422
- Ceres seq_id 1498430
- Location of start within SEQ ID NO 419: at 59 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 4929
- gi No. 2982456
- % Identity 100
- Alignment Length 371
- Location of Alignment in SEQ ID NO 422: from 1 to 367

Maximum Length Sequence corresponding to clone ID 112880

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 423
- Ceres seq_id 1498431

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 424

- Ceres seq_id 1498432
- Location of start within SEQ ID NO 423: at 116 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4930
- DegT/DnrJ/EryC1/StrS family
- Location within SEQ ID NO 424: from 149 to 452 aa.
- Alignment No. 4931
- Aminotransferases class-II
- Location within SEQ ID NO 424: from 158 to 422 aa.
- Alignment No. 4932
- Aminotransferases class-I
- Location within SEQ ID NO 424: from 72 to 464 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4933
- gi No. 4567201
- % Identity 99.8
- Alignment Length 406
- Location of Alignment in SEQ ID NO 424: from 70 to 475

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 425
- Ceres seq_id 1498433
- Location of start within SEQ ID NO 423: at 257 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4934
- DegT/DnrJ/EryC1/StrS family
- Location within SEQ ID NO 425: from 102 to 405 aa.
- Alignment No. 4935
- Aminotransferases class-II
- Location within SEQ ID NO 425: from 111 to 375 aa.
- Alignment No. 4936
- Aminotransferases class-I
- Location within SEQ ID NO 425: from 25 to 417 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4937
- gi No. 4567201
- % Identity 99.8
- Alignment Length 406
- Location of Alignment in SEQ ID NO 425: from 23 to 428

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 426
- Ceres seq_id 1498434
- Location of start within SEQ ID NO 423: at 278 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4938
- DegT/DnrJ/EryC1/StrS family
- Location within SEQ ID NO 426: from 95 to 398 aa.

- Alignment No. 4939
- Aminotransferases class-II
- Location within SEQ ID NO 426: from 104 to 368 aa.
- Alignment No. 4940
- Aminotransferases class-I
- Location within SEQ ID NO 426: from 18 to 410 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4941
- gi No. 4567201
- % Identity 99.8
- Alignment Length 406
- Location of Alignment in SEQ ID NO 426: from 16 to 421

Maximum Length Sequence corresponding to clone ID 113073

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 427
- Ceres seq_id 1498435

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 428
- Ceres seq_id 1498436
- Location of start within SEQ ID NO 427: at 122 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4942
- Ribosomal protein L30
- Location within SEQ ID NO 428: from 84 to 136 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4943
- gi No. 3212879
- % Identity 89.1
- Alignment Length 247
- Location of Alignment in SEQ ID NO 428: from 1 to 244
- Alignment No. 4944
- gi No. 3914772
- % Identity 84
- Alignment Length 100
- Location of Alignment in SEQ ID NO 428: from 5 to 104
- Alignment No. 4945
- gi No. 4262232
- % Identity 90.8
- Alignment Length 240
- Location of Alignment in SEQ ID NO 428: from 5 to 244
- Alignment No. 4946
- gi No. 445613
- % Identity 83.3
- Alignment Length 240
- Location of Alignment in SEQ ID NO 428: from 5 to 244
- Alignment No. 4947
- gi No. 53912
- % Identity 72.7
- Alignment Length 154
- Location of Alignment in SEQ ID NO 428: from 91 to 244

Maximum Length Sequence corresponding to clone ID 113419

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 429
- Ceres seq_id 1498437

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 430
- Ceres seq_id 1498438
- Location of start within SEQ ID NO 429: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4948
- Thioredoxin
- Location within SEQ ID NO 430: from 211 to 320 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4949
- gi No. 1076496
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 430: from 231 to 246
- Alignment No. 4950
- gi No. 99991
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 430: from 233 to 252

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 431
- Ceres seq_id 1498439
- Location of start within SEQ ID NO 429: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4951
- Thioredoxin
- Location within SEQ ID NO 431: from 172 to 281 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4952
- gi No. 1076496
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 431: from 192 to 207
- Alignment No. 4953
- gi No. 99991
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 431: from 194 to 213

Maximum Length Sequence corresponding to clone ID 113834

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 432
- Ceres seq_id 1498440

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 433
- Ceres seq_id 1498441
- Location of start within SEQ ID NO 432: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 4954
- Pyruvate kinase
- Location within SEQ ID NO 433: from 44 to 533 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4955
- gi No. 125606
- % Identity 86.9
- Alignment Length 510
- Location of Alignment in SEQ ID NO 433: from 25 to 534
- Alignment No. 4956
- gi No. 2497538
- % Identity 86.9
- Alignment Length 511
- Location of Alignment in SEQ ID NO 433: from 25 to 534
- Alignment No. 4957
- gi No. 2497543
- % Identity 78.2
- Alignment Length 491
- Location of Alignment in SEQ ID NO 433: from 44 to 534
- Alignment No. 4958
- gi No. 322787
- % Identity 87.1
- Alignment Length 510
- Location of Alignment in SEQ ID NO 433: from 25 to 534
- Alignment No. 4959
- gi No. 4033431
- % Identity 77.6
- Alignment Length 491
- Location of Alignment in SEQ ID NO 433: from 44 to 534
- Alignment No. 4960
- gi No. 585372
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 433: from 45 to 55
- Alignment No. 4961
- gi No. 90134
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 433: from 337 to 370
- Alignment No. 4962
- gi No. 96352
- % Identity 81.5
- Alignment Length 27
- Location of Alignment in SEQ ID NO 433: from 336 to 362

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 434
- Ceres seq_id 1498442
- Location of start within SEQ ID NO 432: at 75 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 4963
- Pyruvate kinase
- Location within SEQ ID NO 434: from 20 to 509 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4964
- gi No. 125606
- % Identity 86.9
- Alignment Length 510
- Location of Alignment in SEQ ID NO 434: from 1 to 510
- Alignment No. 4965
- gi No. 2497538
- % Identity 86.9
- Alignment Length 511
- Location of Alignment in SEQ ID NO 434: from 1 to 510
- Alignment No. 4966
- gi No. 2497543
- % Identity 78.2
- Alignment Length 491
- Location of Alignment in SEQ ID NO 434: from 20 to 510
- Alignment No. 4967
- gi No. 322787
- % Identity 87.1
- Alignment Length 510
- Location of Alignment in SEQ ID NO 434: from 1 to 510
- Alignment No. 4968
- gi No. 4033431
- % Identity 77.6
- Alignment Length 491
- Location of Alignment in SEQ ID NO 434: from 20 to 510
- Alignment No. 4969
- gi No. 585372
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 434: from 21 to 31
- Alignment No. 4970
- gi No. 90134
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 434: from 313 to 346
- Alignment No. 4971
- gi No. 96352
- % Identity 81.5
- Alignment Length 27
- Location of Alignment in SEQ ID NO 434: from 312 to 338

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 435
- Ceres seq_id 1498443
- Location of start within SEQ ID NO 432: at 183 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 4972
- Pyruvate kinase
- Location within SEQ ID NO 435: from 1 to 473 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4973
- gi No. 125606
- % Identity 86.9
- Alignment Length 510
- Location of Alignment in SEQ ID NO 435: from 1 to 474
- Alignment No. 4974
- gi No. 2497538
- % Identity 86.9
- Alignment Length 511
- Location of Alignment in SEQ ID NO 435: from 1 to 474
- Alignment No. 4975
- gi No. 2497543
- % Identity 78.2
- Alignment Length 491
- Location of Alignment in SEQ ID NO 435: from 1 to 474
- Alignment No. 4976
- gi No. 322787
- % Identity 87.1
- Alignment Length 510
- Location of Alignment in SEQ ID NO 435: from 1 to 474
- Alignment No. 4977
- gi No. 4033431
- % Identity 77.6
- Alignment Length 491
- Location of Alignment in SEQ ID NO 435: from 1 to 474
- Alignment No. 4978
- gi No. 90134
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 435: from 277 to 310
- Alignment No. 4979
- gi No. 96352
- % Identity 81.5
- Alignment Length 27
- Location of Alignment in SEQ ID NO 435: from 276 to 302

Maximum Length Sequence corresponding to clone ID 113984

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 436
- Ceres seq_id 1498448

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 437
- Ceres seq_id 1498449
- Location of start within SEQ ID NO 436: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 4980
- gi No. 2213643
- % Identity 75
- Alignment Length 392
- Location of Alignment in SEQ ID NO 437: from 3 to 394

- Alignment No. 4981
- gi No. 498038
- % Identity 72.3
- Alignment Length 321
- Location of Alignment in SEQ ID NO 437: from 2 to 322

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 438
- Ceres seq_id 1498450
- Location of start within SEQ ID NO 436: at 77 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 4982
- gi No. 2213643
- % Identity 75
- Alignment Length 392
- Location of Alignment in SEQ ID NO 438: from 1 to 369
- Alignment No. 4983
- gi No. 498038
- % Identity 72.3
- Alignment Length 321
- Location of Alignment in SEQ ID NO 438: from 1 to 297

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 439
- Ceres seq_id 1498451
- Location of start within SEQ ID NO 436: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 4984
- gi No. 2213643
- % Identity 75
- Alignment Length 392
- Location of Alignment in SEQ ID NO 439: from 1 to 361
- Alignment No. 4985
- gi No. 498038
- % Identity 72.3
- Alignment Length 321
- Location of Alignment in SEQ ID NO 439: from 1 to 289

Maximum Length Sequence corresponding to clone ID 113990

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 440
- Ceres seq_id 1498452

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 441
- Ceres seq_id 1498453
- Location of start within SEQ ID NO 440: at 789 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 4986
- gi No. 4926830
- % Identity 97.7
- Alignment Length 383
- Location of Alignment in SEQ ID NO 441: from 1 to 165

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 442
- Ceres seq_id 1498454
- Location of start within SEQ ID NO 440: at 795 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 4987
- gi No. 4926830
- % Identity 97.7
- Alignment Length 383
- Location of Alignment in SEQ ID NO 442: from 1 to 163

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 443
- Ceres seq_id 1498455
- Location of start within SEQ ID NO 440: at 813 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 4988
- gi No. 4926830
- % Identity 97.7
- Alignment Length 383
- Location of Alignment in SEQ ID NO 443: from 1 to 157

Maximum Length Sequence corresponding to clone ID 114173

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 444
- Ceres seq_id 1498456

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 445
- Ceres seq_id 1498457
- Location of start within SEQ ID NO 444: at 373 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 4989
- Ribosomal protein S7e
- Location within SEQ ID NO 445: from 20 to 93 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4990
- gi No. 3080373
- % Identity 93.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 445: from 1 to 93

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 446

- Ceres seq_id 1498458
- Location of start within SEQ ID NO 444: at 493 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 4991
- Ribosomal protein S7e
- Location within SEQ ID NO 446: from 1 to 53 aa.

(D) Related Amino Acid Sequences

- Alignment No. 4992
- gi No. 3080373
- % Identity 93.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 446: from 1 to 53

Maximum Length Sequence corresponding to clone ID 114302

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 447
- Ceres seq_id 1498459

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 448
- Ceres seq_id 1498460
- Location of start within SEQ ID NO 447: at 82 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 4993
- gi No. 3033397
- % Identity 77.3
- Alignment Length 196
- Location of Alignment in SEQ ID NO 448: from 18 to 209

- Alignment No. 4994
- gi No. 4982522
- % Identity 72.9
- Alignment Length 49
- Location of Alignment in SEQ ID NO 448: from 163 to 210

- Alignment No. 4995
- gi No. 4982522
- % Identity 100
- Alignment Length 138
- Location of Alignment in SEQ ID NO 448: from 1 to 138

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 449
- Ceres seq_id 1498461
- Location of start within SEQ ID NO 447: at 803 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 4996
- gi No. 3033397
- % Identity 88
- Alignment Length 317
- Location of Alignment in SEQ ID NO 449: from 1 to 266

- Alignment No. 4997

- gi No. 4982522
- % Identity 94
- Alignment Length 317
- Location of Alignment in SEQ ID NO 449: from 1 to 266

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 450
- Ceres seq_id 1498462
- Location of start within SEQ ID NO 447: at 890 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 4998
- gi No. 3033397
- % Identity 88
- Alignment Length 317
- Location of Alignment in SEQ ID NO 450: from 1 to 237
- Alignment No. 4999
- gi No. 4982522
- % Identity 94
- Alignment Length 317
- Location of Alignment in SEQ ID NO 450: from 1 to 237

Maximum Length Sequence corresponding to clone ID 114858

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 451
- Ceres seq_id 1498471

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 452
- Ceres seq_id 1498472
- Location of start within SEQ ID NO 451: at 368 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5000
- gi No. 1279640
- % Identity 80.7
- Alignment Length 114
- Location of Alignment in SEQ ID NO 452: from 1 to 79
- Alignment No. 5001
- gi No. 1321924
- % Identity 79.8
- Alignment Length 114
- Location of Alignment in SEQ ID NO 452: from 1 to 79
- Alignment No. 5002
- gi No. 1345504
- % Identity 70.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 452: from 7 to 78
- Alignment No. 5003
- gi No. 1944132
- % Identity 79.8
- Alignment Length 114
- Location of Alignment in SEQ ID NO 452: from 1 to 79

- (B) Polypeptide Sequence

- (C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- ```
- Alignment No. 5006
- gi No. 1321924
- % Identity 79.8
- Alignment Length 114
- Location of Alignment in SEQ ID NO 453: from 1 to 76
```

- ```
- Alignment No. 5007
- gi No. 1345504
- % Identity 70.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 453: from 4 to 75
```

- ```
- Alignment No. 5008
- gi No. 1944132
- % Identity 79.8
- Alignment Length 114
- Location of Alignment in SEQ ID NO 453: from 1 to 76
```

- ```
- Alignment No. 5009
- gi No. 4337200
- % Identity 70.9
- Alignment Length 117
- Location of Alignment in SEQ ID NO 453: from 1 to 79
```

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 454
- Ceres seq_id 1498474
- Location of start within SEQ ID NO 451: at 952 nt.
```

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 115543

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 455
- Ceres seq id 1498475

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 456
- Ceres seq\_id 1498476
- Location of start within SEQ ID NO 455: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5010
- gi No. 2529683
- % Identity 75.1
- Alignment Length 214
- Location of Alignment in SEQ ID NO 456: from 26 to 203
  
- Alignment No. 5011
- gi No. 2529683
- % Identity 74.2
- Alignment Length 452
- Location of Alignment in SEQ ID NO 456: from 128 to 203

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 457
- Ceres seq\_id 1498477
- Location of start within SEQ ID NO 455: at 76 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5012
- gi No. 2529683
- % Identity 75.1
- Alignment Length 214
- Location of Alignment in SEQ ID NO 457: from 1 to 178
  
- Alignment No. 5013
- gi No. 2529683
- % Identity 74.2
- Alignment Length 452
- Location of Alignment in SEQ ID NO 457: from 103 to 178

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 458
- Ceres seq\_id 1498478
- Location of start within SEQ ID NO 455: at 925 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5014
- gi No. 2529683
- % Identity 74.2
- Alignment Length 452
- Location of Alignment in SEQ ID NO 458: from 1 to 269

Maximum Length Sequence corresponding to clone ID 115978

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 459
- Ceres seq\_id 1498487

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 460
- Ceres seq\_id 1498488
- Location of start within SEQ ID NO 459: at 382 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 5015
- Homeobox domain
- Location within SEQ ID NO 460: from 72 to 126 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5016
- gi No. 1076569
- % Identity 72.3
- Alignment Length 94
- Location of Alignment in SEQ ID NO 460: from 71 to 164
- Alignment No. 5017
- gi No. 1076569
- % Identity 71.4
- Alignment Length 98
- Location of Alignment in SEQ ID NO 460: from 71 to 168
- Alignment No. 5018
- gi No. 1076570
- % Identity 78.9
- Alignment Length 95
- Location of Alignment in SEQ ID NO 460: from 70 to 164
- Alignment No. 5019
- gi No. 1168546
- % Identity 98.1
- Alignment Length 312
- Location of Alignment in SEQ ID NO 460: from 1 to 312
- Alignment No. 5020
- gi No. 2661821
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 460: from 111 to 125
- Alignment No. 5021
- gi No. 349263
- % Identity 76.1
- Alignment Length 46
- Location of Alignment in SEQ ID NO 460: from 71 to 116
- Alignment No. 5022
- gi No. 349381
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 460: from 71 to 116

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 461
- Ceres seq\_id 1498489
- Location of start within SEQ ID NO 459: at 517 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5023
- Homeobox domain
- Location within SEQ ID NO 461: from 27 to 81 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5024
- gi No. 1076569

- % Identity 72.3
- Alignment Length 94
- Location of Alignment in SEQ ID NO 461: from 26 to 119
  
- Alignment No. 5025
- gi No. 1076569
- % Identity 71.4
- Alignment Length 98
- Location of Alignment in SEQ ID NO 461: from 26 to 123
  
- Alignment No. 5026
- gi No. 1076570
- % Identity 78.9
- Alignment Length 95
- Location of Alignment in SEQ ID NO 461: from 25 to 119
  
- Alignment No. 5027
- gi No. 1168546
- % Identity 98.1
- Alignment Length 312
- Location of Alignment in SEQ ID NO 461: from 1 to 267
  
- Alignment No. 5028
- gi No. 2661821
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 461: from 66 to 80
  
- Alignment No. 5029
- gi No. 349263
- % Identity 76.1
- Alignment Length 46
- Location of Alignment in SEQ ID NO 461: from 26 to 71
  
- Alignment No. 5030
- gi No. 349381
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 461: from 26 to 71

Maximum Length Sequence corresponding to clone ID 116238

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 462
- Ceres seq\_id 1498493

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 463
- Ceres seq\_id 1498494
- Location of start within SEQ ID NO 462: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5031
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 463: from 83 to 210 aa.
  
- Alignment No. 5032
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 463: from 87 to 210 aa.
  
- Alignment No. 5033
- Eukaryotic DNA topoisomerase I

- Location within SEQ ID NO 463: from 116 to 210 aa.
- Alignment No. 5034
- 11-S plant seed storage protein
- Location within SEQ ID NO 463: from 123 to 210 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 464
- Ceres seq\_id 1498495
- Location of start within SEQ ID NO 462: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5035
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 464: from 63 to 190 aa.
- Alignment No. 5036
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 464: from 67 to 190 aa.
- Alignment No. 5037
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 464: from 96 to 190 aa.
- Alignment No. 5038
- 11-S plant seed storage protein
- Location within SEQ ID NO 464: from 103 to 190 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 465
- Ceres seq\_id 1498496
- Location of start within SEQ ID NO 462: at 119 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5039
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 465: from 44 to 171 aa.
- Alignment No. 5040
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 465: from 48 to 171 aa.
- Alignment No. 5041
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 465: from 77 to 171 aa.
- Alignment No. 5042
- 11-S plant seed storage protein
- Location within SEQ ID NO 465: from 84 to 171 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 116246

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 466

- Ceres seq\_id 1498497

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 467
- Ceres seq\_id 1498498
- Location of start within SEQ ID NO 466: at 329 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5043
- gi No. 4512685
- % Identity 76.8
- Alignment Length 242
- Location of Alignment in SEQ ID NO 467: from 1 to 241

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 468
- Ceres seq\_id 1498499
- Location of start within SEQ ID NO 466: at 593 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5044
- gi No. 4512685
- % Identity 76.8
- Alignment Length 242
- Location of Alignment in SEQ ID NO 468: from 1 to 153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 469
- Ceres seq\_id 1498500
- Location of start within SEQ ID NO 466: at 635 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5045
- gi No. 4512685
- % Identity 76.8
- Alignment Length 242
- Location of Alignment in SEQ ID NO 469: from 1 to 139

Maximum Length Sequence corresponding to clone ID 116626

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 470
- Ceres seq\_id 1498501

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 471
- Ceres seq\_id 1498502
- Location of start within SEQ ID NO 470: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 472
- Ceres seq\_id 1498503
- Location of start within SEQ ID NO 470: at 67 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5046
- Stathmin family
- Location within SEQ ID NO 472: from 73 to 190 aa.
- Alignment No. 5047
- Clathrin light chain
- Location within SEQ ID NO 472: from 2 to 226 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5048
- gi No. 2088662
- % Identity 100
- Alignment Length 258
- Location of Alignment in SEQ ID NO 472: from 1 to 258

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 473
- Ceres seq\_id 1498504
- Location of start within SEQ ID NO 470: at 313 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5049
- Stathmin family
- Location within SEQ ID NO 473: from 1 to 108 aa.
- Alignment No. 5050
- Clathrin light chain
- Location within SEQ ID NO 473: from 1 to 144 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5051
- gi No. 2088662
- % Identity 100
- Alignment Length 258
- Location of Alignment in SEQ ID NO 473: from 1 to 176

Maximum Length Sequence corresponding to clone ID 117795

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 474
- Ceres seq\_id 1498509

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 475
- Ceres seq\_id 1498510
- Location of start within SEQ ID NO 474: at 164 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5052
- gi No. 1279640
- % Identity 74.3
- Alignment Length 169
- Location of Alignment in SEQ ID NO 475: from 1 to 167
- Alignment No. 5053
- gi No. 1321924
- % Identity 77.4
- Alignment Length 155

- Location of Alignment in SEQ ID NO 475: from 15 to 167
- Alignment No. 5054
- gi No. 1944132
- % Identity 77.9
- Alignment Length 154
- Location of Alignment in SEQ ID NO 475: from 16 to 167

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 476
- Ceres seq\_id 1498511
- Location of start within SEQ ID NO 474: at 203 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5055
- gi No. 1279640
- % Identity 74.3
- Alignment Length 169
- Location of Alignment in SEQ ID NO 476: from 1 to 154
- Alignment No. 5056
- gi No. 1321924
- % Identity 77.4
- Alignment Length 155
- Location of Alignment in SEQ ID NO 476: from 2 to 154
- Alignment No. 5057
- gi No. 1944132
- % Identity 77.9
- Alignment Length 154
- Location of Alignment in SEQ ID NO 476: from 3 to 154

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 477
- Ceres seq\_id 1498512
- Location of start within SEQ ID NO 474: at 353 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5058
- gi No. 1279640
- % Identity 74.3
- Alignment Length 169
- Location of Alignment in SEQ ID NO 477: from 1 to 104
- Alignment No. 5059
- gi No. 1321924
- % Identity 77.4
- Alignment Length 155
- Location of Alignment in SEQ ID NO 477: from 1 to 104
- Alignment No. 5060
- gi No. 1944132
- % Identity 77.9
- Alignment Length 154
- Location of Alignment in SEQ ID NO 477: from 1 to 104

Maximum Length Sequence corresponding to clone ID 118147



(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 478
- Ceres seq\_id 1498517

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 479
- Ceres seq\_id 1498518
- Location of start within SEQ ID NO 478: at 176 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5061
- DnaJ domain
- Location within SEQ ID NO 479: from 115 to 170 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 118337

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 480
- Ceres seq\_id 1498519

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 481
- Ceres seq\_id 1498520
- Location of start within SEQ ID NO 480: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 482
- Ceres seq\_id 1498521
- Location of start within SEQ ID NO 480: at 81 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5062
- Eukaryotic initiation factor 5A hypusine (eIF-5A)
- Location within SEQ ID NO 482: from 11 to 126 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5063
- gi No. 100277
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 482: from 14 to 122
- Alignment No. 5064
- gi No. 124224
- % Identity 86.2
- Alignment Length 123
- Location of Alignment in SEQ ID NO 482: from 1 to 122
- Alignment No. 5065
- gi No. 124226
- % Identity 82.7
- Alignment Length 127
- Location of Alignment in SEQ ID NO 482: from 1 to 126
- Alignment No. 5066
- gi No. 124230

- % Identity 81.3
- Alignment Length 128
- Location of Alignment in SEQ ID NO 482: from 1 to 126
  
- Alignment No. 5067
- gi No. 3024018
- % Identity 78.9
- Alignment Length 128
- Location of Alignment in SEQ ID NO 482: from 1 to 126
  
- Alignment No. 5068
- gi No. 3024019
- % Identity 81.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 482: from 1 to 126
  
- Alignment No. 5069
- gi No. 3024020
- % Identity 81.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 482: from 1 to 126
  
- Alignment No. 5070
- gi No. 3024021
- % Identity 82.7
- Alignment Length 127
- Location of Alignment in SEQ ID NO 482: from 1 to 126
  
- Alignment No. 5071
- gi No. 3024022
- % Identity 84.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 482: from 1 to 126
  
- Alignment No. 5072
- gi No. 3789948
- % Identity 82
- Alignment Length 128
- Location of Alignment in SEQ ID NO 482: from 1 to 126
  
- Alignment No. 5073
- gi No. 5080771
- % Identity 84.9
- Alignment Length 126
- Location of Alignment in SEQ ID NO 482: from 1 to 126

Maximum Length Sequence corresponding to clone ID 118626

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 483
- Ceres seq\_id 1498522

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 484
- Ceres seq\_id 1498523
- Location of start within SEQ ID NO 483: at 67 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5074
- Peroxidase
- Location within SEQ ID NO 484: from 41 to 308 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5075
- gi No. 1076635
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 484: from 61 to 75
  
- Alignment No. 5076
- gi No. 1402920
- % Identity 97.7
- Alignment Length 308
- Location of Alignment in SEQ ID NO 484: from 1 to 308
  
- Alignment No. 5077
- gi No. 1546704
- % Identity 97.7
- Alignment Length 305
- Location of Alignment in SEQ ID NO 484: from 4 to 308
  
- Alignment No. 5078
- gi No. 2388571
- % Identity 71.8
- Alignment Length 301
- Location of Alignment in SEQ ID NO 484: from 9 to 308

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 485
- Ceres seq\_id 1498524
- Location of start within SEQ ID NO 483: at 76 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5079
- Peroxidase
- Location within SEQ ID NO 485: from 38 to 305 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5080
- gi No. 1076635
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 485: from 58 to 72
  
- Alignment No. 5081
- gi No. 1402920
- % Identity 97.7
- Alignment Length 308
- Location of Alignment in SEQ ID NO 485: from 1 to 305
  
- Alignment No. 5082
- gi No. 1546704
- % Identity 97.7
- Alignment Length 305
- Location of Alignment in SEQ ID NO 485: from 1 to 305
  
- Alignment No. 5083
- gi No. 2388571
- % Identity 71.8
- Alignment Length 301
- Location of Alignment in SEQ ID NO 485: from 6 to 305

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 486
- Ceres seq\_id 1498525
- Location of start within SEQ ID NO 483: at 127 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5084
- Peroxidase
- Location within SEQ ID NO 486: from 21 to 288 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5085
- gi No. 1076635
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 486: from 41 to 55
- Alignment No. 5086
- gi No. 1402920
- % Identity 97.7
- Alignment Length 308
- Location of Alignment in SEQ ID NO 486: from 1 to 288
- Alignment No. 5087
- gi No. 1546704
- % Identity 97.7
- Alignment Length 305
- Location of Alignment in SEQ ID NO 486: from 1 to 288
- Alignment No. 5088
- gi No. 2388571
- % Identity 71.8
- Alignment Length 301
- Location of Alignment in SEQ ID NO 486: from 1 to 288

Maximum Length Sequence corresponding to clone ID 118636

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 487
- Ceres seq\_id 1498526

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 488
- Ceres seq\_id 1498527
- Location of start within SEQ ID NO 487: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5089
- Dihydroorotase-like
- Location within SEQ ID NO 488: from 88 to 246 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 489
- Ceres seq\_id 1498528
- Location of start within SEQ ID NO 487: at 5 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5090

- Dihydroorotase-like
- Location within SEQ ID NO 489: from 87 to 245 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 490
- Ceres seq\_id 1498529
- Location of start within SEQ ID NO 487: at 757 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5091
- Dihydroorotase-like
- Location within SEQ ID NO 490: from 4 to 230 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 118878

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 491
- Ceres seq\_id 1498530

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 492
- Ceres seq\_id 1498531
- Location of start within SEQ ID NO 491: at 46 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5092
- Prion protein
- Location within SEQ ID NO 492: from 24 to 113 aa.
- Alignment No. 5093
- Dehydrins
- Location within SEQ ID NO 492: from 25 to 107 aa.
- Alignment No. 5094
- Dehydrins
- Location within SEQ ID NO 492: from 42 to 107 aa.
- Alignment No. 5095
- Dehydrins
- Location within SEQ ID NO 492: from 50 to 109 aa.
- Alignment No. 5096
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 492: from 48 to 104 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5097
- gi No. 1076731
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 492: from 83 to 105
- Alignment No. 5098
- gi No. 1076731
- % Identity 74.4
- Alignment Length 40
- Location of Alignment in SEQ ID NO 492: from 66 to 104

- Alignment No. 5099
- gi No. 1076731
- % Identity 70.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 492: from 42 to 104
  
- Alignment No. 5100
- gi No. 1150834
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 492: from 44 to 60
  
- Alignment No. 5101
- gi No. 1150834
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 492: from 42 to 58
  
- Alignment No. 5102
- gi No. 1150834
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 492: from 84 to 101
  
- Alignment No. 5103
- gi No. 1150834
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 492: from 45 to 62
  
- Alignment No. 5104
- gi No. 1150834
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 492: from 46 to 63
  
- Alignment No. 5105
- gi No. 121644
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 492: from 53 to 101
  
- Alignment No. 5106
- gi No. 166376
- % Identity 88.9
- Alignment Length 18
- Location of Alignment in SEQ ID NO 492: from 43 to 60
  
- Alignment No. 5107
- gi No. 2047353
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 492: from 83 to 104
  
- Alignment No. 5108
- gi No. 2119042
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 492: from 78 to 104

- Alignment No. 5109
- gi No. 2119043
- % Identity 71
- Alignment Length 33
- Location of Alignment in SEQ ID NO 492: from 78 to 107
  
- Alignment No. 5110
- gi No. 2134839
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 492: from 42 to 56
  
- Alignment No. 5111
- gi No. 2331131
- % Identity 76.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 492: from 77 to 107
  
- Alignment No. 5112
- gi No. 2499130
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 492: from 44 to 60
  
- Alignment No. 5113
- gi No. 2499130
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 492: from 42 to 58
  
- Alignment No. 5114
- gi No. 2499130
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 492: from 84 to 101
  
- Alignment No. 5115
- gi No. 2499130
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 492: from 45 to 62
  
- Alignment No. 5116
- gi No. 2499130
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 492: from 46 to 63
  
- Alignment No. 5117
- gi No. 2674201
- % Identity 71.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 492: from 77 to 104
  
- Alignment No. 5118
- gi No. 2760483
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 492: from 74 to 101
  
- Alignment No. 5119

- gi No. 2826811
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 492: from 82 to 104
  
- Alignment No. 5120
- gi No. 2826811
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 492: from 75 to 101
  
- Alignment No. 5121
- gi No. 2826811
- % Identity 76.7
- Alignment Length 31
- Location of Alignment in SEQ ID NO 492: from 67 to 96
  
- Alignment No. 5122
- gi No. 2961382
- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 492: from 78 to 101
  
- Alignment No. 5123
- gi No. 322514
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 492: from 66 to 104
  
- Alignment No. 5124
- gi No. 322647
- % Identity 72.3
- Alignment Length 68
- Location of Alignment in SEQ ID NO 492: from 42 to 101
  
- Alignment No. 5125
- gi No. 3877954
- % Identity 70
- Alignment Length 31
- Location of Alignment in SEQ ID NO 492: from 74 to 101
  
- Alignment No. 5126
- gi No. 3893085
- % Identity 72
- Alignment Length 26
- Location of Alignment in SEQ ID NO 492: from 42 to 66
  
- Alignment No. 5127
- gi No. 4455314
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 492: from 66 to 104
  
- Alignment No. 5128
- gi No. 4502943
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 492: from 42 to 56
  
- Alignment No. 5129
- gi No. 4507911

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- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 492: from 74 to 101
  
- Alignment No. 5130
- gi No. 4567236
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 492: from 74 to 104
  
- Alignment No. 5131
- gi No. 4581166
- % Identity 72.1
- Alignment Length 65
- Location of Alignment in SEQ ID NO 492: from 44 to 104
  
- Alignment No. 5132
- gi No. 4581173
- % Identity 85.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 492: from 1 to 104
  
- Alignment No. 5133
- gi No. 4581173
- % Identity 78.4
- Alignment Length 125
- Location of Alignment in SEQ ID NO 492: from 1 to 113
  
- Alignment No. 5134
- gi No. 4581180
- % Identity 96.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 492: from 1 to 104
  
- Alignment No. 5135
- gi No. 4581180
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 492: from 1 to 104
  
- Alignment No. 5136
- gi No. 4678224
- % Identity 71.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 492: from 42 to 101
  
- Alignment No. 5137
- gi No. 469072
- % Identity 71
- Alignment Length 33
- Location of Alignment in SEQ ID NO 492: from 78 to 107
  
- Alignment No. 5138
- gi No. 544423
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 492: from 74 to 104
  
- Alignment No. 5139
- gi No. 544423
- % Identity 71.4

- Alignment Length 43
- Location of Alignment in SEQ ID NO 492: from 66 to 104
- Alignment No. 5140
- gi No. 544424
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 492: from 74 to 104
- Alignment No. 5141
- gi No. 544426
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 492: from 83 to 107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 493
- Ceres seq\_id 1498532
- Location of start within SEQ ID NO 491: at 130 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5142
- Prion protein
- Location within SEQ ID NO 493: from 1 to 85 aa.
- Alignment No. 5143
- Dehydrins
- Location within SEQ ID NO 493: from 1 to 79 aa.
- Alignment No. 5144
- Dehydrins
- Location within SEQ ID NO 493: from 14 to 79 aa.
- Alignment No. 5145
- Dehydrins
- Location within SEQ ID NO 493: from 22 to 81 aa.
- Alignment No. 5146
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 493: from 20 to 76 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5147
- gi No. 1076731
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 493: from 55 to 77
- Alignment No. 5148
- gi No. 1076731
- % Identity 74.4
- Alignment Length 40
- Location of Alignment in SEQ ID NO 493: from 38 to 76
- Alignment No. 5149
- gi No. 1076731
- % Identity 70.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 493: from 14 to 76

- Alignment No. 5150
- gi No. 1150834
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 493: from 16 to 32
  
- Alignment No. 5151
- gi No. 1150834
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 493: from 14 to 30
  
- Alignment No. 5152
- gi No. 1150834
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 493: from 56 to 73
  
- Alignment No. 5153
- gi No. 1150834
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 493: from 17 to 34
  
- Alignment No. 5154
- gi No. 1150834
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 493: from 18 to 35
  
- Alignment No. 5155
- gi No. 121644
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 493: from 25 to 73
  
- Alignment No. 5156
- gi No. 166376
- % Identity 88.9
- Alignment Length 18
- Location of Alignment in SEQ ID NO 493: from 15 to 32
  
- Alignment No. 5157
- gi No. 2047353
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 493: from 55 to 76
  
- Alignment No. 5158
- gi No. 2119042
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 493: from 50 to 76
  
- Alignment No. 5159
- gi No. 2119043
- % Identity 71
- Alignment Length 33
- Location of Alignment in SEQ ID NO 493: from 50 to 79
  
- Alignment No. 5160

- gi No. 2134839
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 493: from 14 to 28
  
- Alignment No. 5161
- gi No. 2331131
- % Identity 76.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 493: from 49 to 79
  
- Alignment No. 5162
- gi No. 2499130
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 493: from 16 to 32
  
- Alignment No. 5163
- gi No. 2499130
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 493: from 14 to 30
  
- Alignment No. 5164
- gi No. 2499130
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 493: from 56 to 73
  
- Alignment No. 5165
- gi No. 2499130
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 493: from 17 to 34
  
- Alignment No. 5166
- gi No. 2499130
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 493: from 18 to 35
  
- Alignment No. 5167
- gi No. 2674201
- % Identity 71.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 493: from 49 to 76
  
- Alignment No. 5168
- gi No. 2760483
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 493: from 46 to 73
  
- Alignment No. 5169
- gi No. 2826811
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 493: from 54 to 76
  
- Alignment No. 5170
- gi No. 2826811

- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 493: from 47 to 73
  
- Alignment No. 5171
- gi No. 2826811
- % Identity 76.7
- Alignment Length 31
- Location of Alignment in SEQ ID NO 493: from 39 to 68
  
- Alignment No. 5172
- gi No. 2961382
- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 493: from 50 to 73
  
- Alignment No. 5173
- gi No. 322514
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 493: from 38 to 76
  
- Alignment No. 5174
- gi No. 322647
- % Identity 72.3
- Alignment Length 68
- Location of Alignment in SEQ ID NO 493: from 14 to 73
  
- Alignment No. 5175
- gi No. 3877954
- % Identity 70
- Alignment Length 31
- Location of Alignment in SEQ ID NO 493: from 46 to 73
  
- Alignment No. 5176
- gi No. 3893085
- % Identity 72
- Alignment Length 26
- Location of Alignment in SEQ ID NO 493: from 14 to 38
  
- Alignment No. 5177
- gi No. 4455314
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 493: from 38 to 76
  
- Alignment No. 5178
- gi No. 4502943
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 493: from 14 to 28
  
- Alignment No. 5179
- gi No. 4507911
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 493: from 46 to 73
  
- Alignment No. 5180
- gi No. 4567236
- % Identity 71.9

- Alignment Length 32
- Location of Alignment in SEQ ID NO 493: from 46 to 76
  
- Alignment No. 5181
- gi No. 4581166
- % Identity 72.1
- Alignment Length 65
- Location of Alignment in SEQ ID NO 493: from 16 to 76
  
- Alignment No. 5182
- gi No. 4581173
- % Identity 85.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 493: from 1 to 76
  
- Alignment No. 5183
- gi No. 4581173
- % Identity 78.4
- Alignment Length 125
- Location of Alignment in SEQ ID NO 493: from 1 to 85
  
- Alignment No. 5184
- gi No. 4581180
- % Identity 96.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 493: from 1 to 76
  
- Alignment No. 5185
- gi No. 4581180
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 493: from 1 to 76
  
- Alignment No. 5186
- gi No. 4678224
- % Identity 71.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 493: from 14 to 73
  
- Alignment No. 5187
- gi No. 469072
- % Identity 71
- Alignment Length 33
- Location of Alignment in SEQ ID NO 493: from 50 to 79
  
- Alignment No. 5188
- gi No. 544423
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 493: from 46 to 76
  
- Alignment No. 5189
- gi No. 544423
- % Identity 71.4
- Alignment Length 43
- Location of Alignment in SEQ ID NO 493: from 38 to 76
  
- Alignment No. 5190
- gi No. 544424
- % Identity 71.9
- Alignment Length 32

- Location of Alignment in SEQ ID NO 493: from 46 to 76
- Alignment No. 5191
- gi No. 544426
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 493: from 55 to 79

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 494
- Ceres seq\_id 1498533
- Location of start within SEQ ID NO 491: at 173 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 119070

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 495
- Ceres seq\_id 1498534

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 496
- Ceres seq\_id 1498535
- Location of start within SEQ ID NO 495: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5192
- Aldehyde dehydrogenase
- Location within SEQ ID NO 496: from 12 to 444 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 497
- Ceres seq\_id 1498536
- Location of start within SEQ ID NO 495: at 193 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5193
- Aldehyde dehydrogenase
- Location within SEQ ID NO 497: from 1 to 403 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 498
- Ceres seq\_id 1498537
- Location of start within SEQ ID NO 495: at 337 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5194
- Aldehyde dehydrogenase
- Location within SEQ ID NO 498: from 1 to 355 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 119288

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 499
- Ceres seq\_id 1498542

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 500
- Ceres seq\_id 1498543
- Location of start within SEQ ID NO 499: at 105 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5195
- Major intrinsic protein
- Location within SEQ ID NO 500: from 13 to 166 aa.
- Alignment No. 5196
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 500: from 165 to 256 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5197
- gi No. 1002803
- % Identity 100
- Alignment Length 140
- Location of Alignment in SEQ ID NO 500: from 165 to 304
- Alignment No. 5198
- gi No. 1076502
- % Identity 85.7
- Alignment Length 126
- Location of Alignment in SEQ ID NO 500: from 165 to 290
- Alignment No. 5199
- gi No. 1170891
- % Identity 76.9
- Alignment Length 121
- Location of Alignment in SEQ ID NO 500: from 1 to 121
- Alignment No. 5200
- gi No. 1200161
- % Identity 75.9
- Alignment Length 166
- Location of Alignment in SEQ ID NO 500: from 1 to 166
- Alignment No. 5201
- gi No. 120229
- % Identity 82.4
- Alignment Length 125
- Location of Alignment in SEQ ID NO 500: from 165 to 289
- Alignment No. 5202
- gi No. 126962
- % Identity 98.8
- Alignment Length 166
- Location of Alignment in SEQ ID NO 500: from 1 to 166
- Alignment No. 5203
- gi No. 135860
- % Identity 99.4
- Alignment Length 166
- Location of Alignment in SEQ ID NO 500: from 1 to 166



- Alignment No. 5204
- gi No. 1364117
- % Identity 81.8
- Alignment Length 132
- Location of Alignment in SEQ ID NO 500: from 165 to 296
- Alignment No. 5205
- gi No. 1514977
- % Identity 89.8
- Alignment Length 167
- Location of Alignment in SEQ ID NO 500: from 1 to 166
- Alignment No. 5206
- gi No. 1549339
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 500: from 142 to 166
- Alignment No. 5207
- gi No. 1622729
- % Identity 79.4
- Alignment Length 165
- Location of Alignment in SEQ ID NO 500: from 1 to 165
- Alignment No. 5208
- gi No. 1729971
- % Identity 78.3
- Alignment Length 166
- Location of Alignment in SEQ ID NO 500: from 1 to 166
- Alignment No. 5209
- gi No. 1786049
- % Identity 80.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 500: from 165 to 304
- Alignment No. 5210
- gi No. 1928981
- % Identity 92.8
- Alignment Length 166
- Location of Alignment in SEQ ID NO 500: from 1 to 166
- Alignment No. 5211
- gi No. 1928983
- % Identity 92.2
- Alignment Length 90
- Location of Alignment in SEQ ID NO 500: from 77 to 166
- Alignment No. 5212
- gi No. 1944197
- % Identity 79.1
- Alignment Length 134
- Location of Alignment in SEQ ID NO 500: from 165 to 298
- Alignment No. 5213
- gi No. 2129856
- % Identity 84.9
- Alignment Length 126
- Location of Alignment in SEQ ID NO 500: from 165 to 290
- Alignment No. 5214

- gi No. 2246621
- % Identity 87
- Alignment Length 108
- Location of Alignment in SEQ ID NO 500: from 59 to 166
  
- Alignment No. 5215
- gi No. 2344781
- % Identity 80.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 500: from 165 to 304
  
- Alignment No. 5216
- gi No. 2443836
- % Identity 72.5
- Alignment Length 180
- Location of Alignment in SEQ ID NO 500: from 1 to 178
  
- Alignment No. 5217
- gi No. 2465434
- % Identity 81.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 500: from 165 to 304
  
- Alignment No. 5218
- gi No. 2801407
- % Identity 80
- Alignment Length 140
- Location of Alignment in SEQ ID NO 500: from 165 to 304
  
- Alignment No. 5219
- gi No. 2828006
- % Identity 80
- Alignment Length 140
- Location of Alignment in SEQ ID NO 500: from 165 to 304
  
- Alignment No. 5220
- gi No. 282962
- % Identity 81.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 500: from 165 to 304
  
- Alignment No. 5221
- gi No. 3004950
- % Identity 74.7
- Alignment Length 166
- Location of Alignment in SEQ ID NO 500: from 1 to 166
  
- Alignment No. 5222
- gi No. 3021538
- % Identity 71.1
- Alignment Length 166
- Location of Alignment in SEQ ID NO 500: from 1 to 166
  
- Alignment No. 5223
- gi No. 322664
- % Identity 93.6
- Alignment Length 140
- Location of Alignment in SEQ ID NO 500: from 165 to 304
  
- Alignment No. 5224
- gi No. 3298460

- % Identity 71
- Alignment Length 100
- Location of Alignment in SEQ ID NO 500: from 81 to 178
  
- Alignment No. 5225
- gi No. 3298468
- % Identity 83.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 500: from 81 to 166
  
- Alignment No. 5226
- gi No. 3688799
- % Identity 80.8
- Alignment Length 172
- Location of Alignment in SEQ ID NO 500: from 1 to 171
  
- Alignment No. 5227
- gi No. 3695375
- % Identity 71.7
- Alignment Length 180
- Location of Alignment in SEQ ID NO 500: from 1 to 178
  
- Alignment No. 5228
- gi No. 3790548
- % Identity 99.3
- Alignment Length 140
- Location of Alignment in SEQ ID NO 500: from 165 to 304
  
- Alignment No. 5229
- gi No. 3790550
- % Identity 100
- Alignment Length 29
- Location of Alignment in SEQ ID NO 500: from 165 to 193
  
- Alignment No. 5230
- gi No. 4099406
- % Identity 72.9
- Alignment Length 166
- Location of Alignment in SEQ ID NO 500: from 1 to 166
  
- Alignment No. 5231
- gi No. 4126401
- % Identity 81.3
- Alignment Length 144
- Location of Alignment in SEQ ID NO 500: from 165 to 304
  
- Alignment No. 5232
- gi No. 4138262
- % Identity 75.3
- Alignment Length 166
- Location of Alignment in SEQ ID NO 500: from 1 to 166
  
- Alignment No. 5233
- gi No. 4512589
- % Identity 79.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 500: from 165 to 304
  
- Alignment No. 5234
- gi No. 4512591
- % Identity 78.4

- Alignment Length 148
- Location of Alignment in SEQ ID NO 500: from 165 to 304
- Alignment No. 5235
- gi No. 4512593
- % Identity 78.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 500: from 165 to 304
- Alignment No. 5236
- gi No. 4539145
- % Identity 72.1
- Alignment Length 165
- Location of Alignment in SEQ ID NO 500: from 1 to 165
- Alignment No. 5237
- gi No. 453980
- % Identity 70.3
- Alignment Length 176
- Location of Alignment in SEQ ID NO 500: from 5 to 178
- Alignment No. 5238
- gi No. 467996
- % Identity 78.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 500: from 165 to 304
- Alignment No. 5239
- gi No. 475048
- % Identity 99.4
- Alignment Length 166
- Location of Alignment in SEQ ID NO 500: from 1 to 166
- Alignment No. 5240
- gi No. 4884866
- % Identity 70
- Alignment Length 180
- Location of Alignment in SEQ ID NO 500: from 1 to 178
- Alignment No. 5241
- gi No. 5081419
- % Identity 88.6
- Alignment Length 167
- Location of Alignment in SEQ ID NO 500: from 1 to 166
- Alignment No. 5242
- gi No. 5139543
- % Identity 74.3
- Alignment Length 180
- Location of Alignment in SEQ ID NO 500: from 1 to 178
- Alignment No. 5243
- gi No. 541950
- % Identity 73
- Alignment Length 180
- Location of Alignment in SEQ ID NO 500: from 1 to 178
- Alignment No. 5244
- gi No. 541951
- % Identity 73.9
- Alignment Length 180

- Location of Alignment in SEQ ID NO 500: from 1 to 178
- Alignment No. 5245
- gi No. 629784
- % Identity 71.1
- Alignment Length 166
- Location of Alignment in SEQ ID NO 500: from 1 to 166
- Alignment No. 5246
- gi No. 727411
- % Identity 81.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 500: from 165 to 297
- Alignment No. 5247
- gi No. 729503
- % Identity 80
- Alignment Length 140
- Location of Alignment in SEQ ID NO 500: from 165 to 304
- Alignment No. 5248
- gi No. 729504
- % Identity 78.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 500: from 165 to 304
- Alignment No. 5249
- gi No. 729505
- % Identity 82.1
- Alignment Length 145
- Location of Alignment in SEQ ID NO 500: from 165 to 304
- Alignment No. 5250
- gi No. 729506
- % Identity 93.6
- Alignment Length 140
- Location of Alignment in SEQ ID NO 500: from 165 to 304
- Alignment No. 5251
- gi No. 729507
- % Identity 81.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 500: from 165 to 304
- Alignment No. 5252
- gi No. 729508
- % Identity 83.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 500: from 165 to 304

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 501
- Ceres seq\_id 1498544
- Location of start within SEQ ID NO 499: at 228 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5253
- Major intrinsic protein
- Location within SEQ ID NO 501: from 1 to 125 aa.

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- Alignment No. 5254
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 501: from 124 to 215 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5255
- gi No. 1002803
- % Identity 100
- Alignment Length 140
- Location of Alignment in SEQ ID NO 501: from 124 to 263
- Alignment No. 5256
- gi No. 1076502
- % Identity 85.7
- Alignment Length 126
- Location of Alignment in SEQ ID NO 501: from 124 to 249
- Alignment No. 5257
- gi No. 1170891
- % Identity 76.9
- Alignment Length 121
- Location of Alignment in SEQ ID NO 501: from 1 to 80
- Alignment No. 5258
- gi No. 1200161
- % Identity 75.9
- Alignment Length 166
- Location of Alignment in SEQ ID NO 501: from 1 to 125
- Alignment No. 5259
- gi No. 120229
- % Identity 82.4
- Alignment Length 125
- Location of Alignment in SEQ ID NO 501: from 124 to 248
- Alignment No. 5260
- gi No. 126962
- % Identity 98.8
- Alignment Length 166
- Location of Alignment in SEQ ID NO 501: from 1 to 125
- Alignment No. 5261
- gi No. 135860
- % Identity 99.4
- Alignment Length 166
- Location of Alignment in SEQ ID NO 501: from 1 to 125
- Alignment No. 5262
- gi No. 1364117
- % Identity 81.8
- Alignment Length 132
- Location of Alignment in SEQ ID NO 501: from 124 to 255
- Alignment No. 5263
- gi No. 1514977
- % Identity 89.8
- Alignment Length 167
- Location of Alignment in SEQ ID NO 501: from 1 to 125
- Alignment No. 5264
- gi No. 1549339

- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 501: from 101 to 125
  
- Alignment No. 5265
- gi No. 1622729
- % Identity 79.4
- Alignment Length 165
- Location of Alignment in SEQ ID NO 501: from 1 to 124
  
- Alignment No. 5266
- gi No. 1729971
- % Identity 78.3
- Alignment Length 166
- Location of Alignment in SEQ ID NO 501: from 1 to 125
  
- Alignment No. 5267
- gi No. 1786049
- % Identity 80.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 501: from 124 to 263
  
- Alignment No. 5268
- gi No. 1928981
- % Identity 92.8
- Alignment Length 166
- Location of Alignment in SEQ ID NO 501: from 1 to 125
  
- Alignment No. 5269
- gi No. 1928983
- % Identity 92.2
- Alignment Length 90
- Location of Alignment in SEQ ID NO 501: from 36 to 125
  
- Alignment No. 5270
- gi No. 1944197
- % Identity 79.1
- Alignment Length 134
- Location of Alignment in SEQ ID NO 501: from 124 to 257
  
- Alignment No. 5271
- gi No. 2129856
- % Identity 84.9
- Alignment Length 126
- Location of Alignment in SEQ ID NO 501: from 124 to 249
  
- Alignment No. 5272
- gi No. 2246621
- % Identity 87
- Alignment Length 108
- Location of Alignment in SEQ ID NO 501: from 18 to 125
  
- Alignment No. 5273
- gi No. 2344781
- % Identity 80.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 501: from 124 to 263
  
- Alignment No. 5274
- gi No. 2443836
- % Identity 72.5

- Alignment Length 180
- Location of Alignment in SEQ ID NO 501: from 1 to 137
  
- Alignment No. 5275
- gi No. 2465434
- % Identity 81.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 501: from 124 to 263
  
- Alignment No. 5276
- gi No. 2801407
- % Identity 80
- Alignment Length 140
- Location of Alignment in SEQ ID NO 501: from 124 to 263
  
- Alignment No. 5277
- gi No. 2828006
- % Identity 80
- Alignment Length 140
- Location of Alignment in SEQ ID NO 501: from 124 to 263
  
- Alignment No. 5278
- gi No. 282962
- % Identity 81.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 501: from 124 to 263
  
- Alignment No. 5279
- gi No. 3004950
- % Identity 74.7
- Alignment Length 166
- Location of Alignment in SEQ ID NO 501: from 1 to 125
  
- Alignment No. 5280
- gi No. 3021538
- % Identity 71.1
- Alignment Length 166
- Location of Alignment in SEQ ID NO 501: from 1 to 125
  
- Alignment No. 5281
- gi No. 322664
- % Identity 93.6
- Alignment Length 140
- Location of Alignment in SEQ ID NO 501: from 124 to 263
  
- Alignment No. 5282
- gi No. 3298460
- % Identity 71
- Alignment Length 100
- Location of Alignment in SEQ ID NO 501: from 40 to 137
  
- Alignment No. 5283
- gi No. 3298468
- % Identity 83.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 501: from 40 to 125
  
- Alignment No. 5284
- gi No. 3688799
- % Identity 80.8
- Alignment Length 172

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- Location of Alignment in SEQ ID NO 501: from 1 to 130
- Alignment No. 5285
- gi No. 3695375
- % Identity 71.7
- Alignment Length 180
- Location of Alignment in SEQ ID NO 501: from 1 to 137
- Alignment No. 5286
- gi No. 3790548
- % Identity 99.3
- Alignment Length 140
- Location of Alignment in SEQ ID NO 501: from 124 to 263
- Alignment No. 5287
- gi No. 3790550
- % Identity 100
- Alignment Length 29
- Location of Alignment in SEQ ID NO 501: from 124 to 152
- Alignment No. 5288
- gi No. 4099406
- % Identity 72.9
- Alignment Length 166
- Location of Alignment in SEQ ID NO 501: from 1 to 125
- Alignment No. 5289
- gi No. 4126401
- % Identity 81.3
- Alignment Length 144
- Location of Alignment in SEQ ID NO 501: from 124 to 263
- Alignment No. 5290
- gi No. 4138262
- % Identity 75.3
- Alignment Length 166
- Location of Alignment in SEQ ID NO 501: from 1 to 125
- Alignment No. 5291
- gi No. 4512589
- % Identity 79.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 501: from 124 to 263
- Alignment No. 5292
- gi No. 4512591
- % Identity 78.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 501: from 124 to 263
- Alignment No. 5293
- gi No. 4512593
- % Identity 78.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 501: from 124 to 263
- Alignment No. 5294
- gi No. 4539145
- % Identity 72.1
- Alignment Length 165
- Location of Alignment in SEQ ID NO 501: from 1 to 124

- Alignment No. 5295
- gi No. 453980
- % Identity 70.3
- Alignment Length 176
- Location of Alignment in SEQ ID NO 501: from 1 to 137
  
- Alignment No. 5296
- gi No. 467996
- % Identity 78.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 501: from 124 to 263
  
- Alignment No. 5297
- gi No. 475048
- % Identity 99.4
- Alignment Length 166
- Location of Alignment in SEQ ID NO 501: from 1 to 125
  
- Alignment No. 5298
- gi No. 4884866
- % Identity 70
- Alignment Length 180
- Location of Alignment in SEQ ID NO 501: from 1 to 137
  
- Alignment No. 5299
- gi No. 5081419
- % Identity 88.6
- Alignment Length 167
- Location of Alignment in SEQ ID NO 501: from 1 to 125
  
- Alignment No. 5300
- gi No. 5139543
- % Identity 74.3
- Alignment Length 180
- Location of Alignment in SEQ ID NO 501: from 1 to 137
  
- Alignment No. 5301
- gi No. 541950
- % Identity 73
- Alignment Length 180
- Location of Alignment in SEQ ID NO 501: from 1 to 137
  
- Alignment No. 5302
- gi No. 541951
- % Identity 73.9
- Alignment Length 180
- Location of Alignment in SEQ ID NO 501: from 1 to 137
  
- Alignment No. 5303
- gi No. 629784
- % Identity 71.1
- Alignment Length 166
- Location of Alignment in SEQ ID NO 501: from 1 to 125
  
- Alignment No. 5304
- gi No. 727411
- % Identity 81.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 501: from 124 to 256

- Alignment No. 5305
- gi No. 729503
- % Identity 80
- Alignment Length 140
- Location of Alignment in SEQ ID NO 501: from 124 to 263
  
- Alignment No. 5306
- gi No. 729504
- % Identity 78.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 501: from 124 to 263
  
- Alignment No. 5307
- gi No. 729505
- % Identity 82.1
- Alignment Length 145
- Location of Alignment in SEQ ID NO 501: from 124 to 263
  
- Alignment No. 5308
- gi No. 729506
- % Identity 93.6
- Alignment Length 140
- Location of Alignment in SEQ ID NO 501: from 124 to 263
  
- Alignment No. 5309
- gi No. 729507
- % Identity 81.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 501: from 124 to 263
  
- Alignment No. 5310
- gi No. 729508
- % Identity 83.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 501: from 124 to 263

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 502
- Ceres seq\_id 1498545
- Location of start within SEQ ID NO 499: at 555 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5311
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 502: from 15 to 106 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5312
- gi No. 1002803
- % Identity 100
- Alignment Length 140
- Location of Alignment in SEQ ID NO 502: from 15 to 154
  
- Alignment No. 5313
- gi No. 1076502
- % Identity 85.7
- Alignment Length 126
- Location of Alignment in SEQ ID NO 502: from 15 to 140
  
- Alignment No. 5314

- gi No. 1200161
- % Identity 75.9
- Alignment Length 166
- Location of Alignment in SEQ ID NO 502: from 1 to 16
  
- Alignment No. 5315
- gi No. 120229
- % Identity 82.4
- Alignment Length 125
- Location of Alignment in SEQ ID NO 502: from 15 to 139
  
- Alignment No. 5316
- gi No. 126962
- % Identity 98.8
- Alignment Length 166
- Location of Alignment in SEQ ID NO 502: from 1 to 16
  
- Alignment No. 5317
- gi No. 135860
- % Identity 99.4
- Alignment Length 166
- Location of Alignment in SEQ ID NO 502: from 1 to 16
  
- Alignment No. 5318
- gi No. 1364117
- % Identity 81.8
- Alignment Length 132
- Location of Alignment in SEQ ID NO 502: from 15 to 146
  
- Alignment No. 5319
- gi No. 1514977
- % Identity 89.8
- Alignment Length 167
- Location of Alignment in SEQ ID NO 502: from 1 to 16
  
- Alignment No. 5320
- gi No. 1549339
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 502: from 1 to 16
  
- Alignment No. 5321
- gi No. 1622729
- % Identity 79.4
- Alignment Length 165
- Location of Alignment in SEQ ID NO 502: from 1 to 15
  
- Alignment No. 5322
- gi No. 1729971
- % Identity 78.3
- Alignment Length 166
- Location of Alignment in SEQ ID NO 502: from 1 to 16
  
- Alignment No. 5323
- gi No. 1786049
- % Identity 80.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 502: from 15 to 154
  
- Alignment No. 5324
- gi No. 1928981

- % Identity 92.8
- Alignment Length 166
- Location of Alignment in SEQ ID NO 502: from 1 to 16
  
- Alignment No. 5325
- gi No. 1928983
- % Identity 92.2
- Alignment Length 90
- Location of Alignment in SEQ ID NO 502: from 1 to 16
  
- Alignment No. 5326
- gi No. 1944197
- % Identity 79.1
- Alignment Length 134
- Location of Alignment in SEQ ID NO 502: from 15 to 148
  
- Alignment No. 5327
- gi No. 2129856
- % Identity 84.9
- Alignment Length 126
- Location of Alignment in SEQ ID NO 502: from 15 to 140
  
- Alignment No. 5328
- gi No. 2246621
- % Identity 87
- Alignment Length 108
- Location of Alignment in SEQ ID NO 502: from 1 to 16
  
- Alignment No. 5329
- gi No. 2344781
- % Identity 80.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 502: from 15 to 154
  
- Alignment No. 5330
- gi No. 2443836
- % Identity 72.5
- Alignment Length 180
- Location of Alignment in SEQ ID NO 502: from 1 to 28
  
- Alignment No. 5331
- gi No. 2465434
- % Identity 81.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 502: from 15 to 154
  
- Alignment No. 5332
- gi No. 2801407
- % Identity 80
- Alignment Length 140
- Location of Alignment in SEQ ID NO 502: from 15 to 154
  
- Alignment No. 5333
- gi No. 2828006
- % Identity 80
- Alignment Length 140
- Location of Alignment in SEQ ID NO 502: from 15 to 154
  
- Alignment No. 5334
- gi No. 282962
- % Identity 81.1

- Alignment Length 148
- Location of Alignment in SEQ ID NO 502: from 15 to 154
  
- Alignment No. 5335
- gi No. 3004950
- % Identity 74.7
- Alignment Length 166
- Location of Alignment in SEQ ID NO 502: from 1 to 16
  
- Alignment No. 5336
- gi No. 3021538
- % Identity 71.1
- Alignment Length 166
- Location of Alignment in SEQ ID NO 502: from 1 to 16
  
- Alignment No. 5337
- gi No. 322664
- % Identity 93.6
- Alignment Length 140
- Location of Alignment in SEQ ID NO 502: from 15 to 154
  
- Alignment No. 5338
- gi No. 3298460
- % Identity 71
- Alignment Length 100
- Location of Alignment in SEQ ID NO 502: from 1 to 28
  
- Alignment No. 5339
- gi No. 3298468
- % Identity 83.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 502: from 1 to 16
  
- Alignment No. 5340
- gi No. 3688799
- % Identity 80.8
- Alignment Length 172
- Location of Alignment in SEQ ID NO 502: from 1 to 21
  
- Alignment No. 5341
- gi No. 3695375
- % Identity 71.7
- Alignment Length 180
- Location of Alignment in SEQ ID NO 502: from 1 to 28
  
- Alignment No. 5342
- gi No. 3790548
- % Identity 99.3
- Alignment Length 140
- Location of Alignment in SEQ ID NO 502: from 15 to 154
  
- Alignment No. 5343
- gi No. 3790550
- % Identity 100
- Alignment Length 29
- Location of Alignment in SEQ ID NO 502: from 15 to 43
  
- Alignment No. 5344
- gi No. 4099406
- % Identity 72.9
- Alignment Length 166

- Location of Alignment in SEQ ID NO 502: from 1 to 16
- Alignment No. 5345
- gi No. 4126401
- % Identity 81.3
- Alignment Length 144
- Location of Alignment in SEQ ID NO 502: from 15 to 154
- Alignment No. 5346
- gi No. 4138262
- % Identity 75.3
- Alignment Length 166
- Location of Alignment in SEQ ID NO 502: from 1 to 16
- Alignment No. 5347
- gi No. 4512589
- % Identity 79.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 502: from 15 to 154
- Alignment No. 5348
- gi No. 4512591
- % Identity 78.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 502: from 15 to 154
- Alignment No. 5349
- gi No. 4512593
- % Identity 78.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 502: from 15 to 154
- Alignment No. 5350
- gi No. 4539145
- % Identity 72.1
- Alignment Length 165
- Location of Alignment in SEQ ID NO 502: from 1 to 15
- Alignment No. 5351
- gi No. 453980
- % Identity 70.3
- Alignment Length 176
- Location of Alignment in SEQ ID NO 502: from 1 to 28
- Alignment No. 5352
- gi No. 467996
- % Identity 78.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 502: from 15 to 154
- Alignment No. 5353
- gi No. 475048
- % Identity 99.4
- Alignment Length 166
- Location of Alignment in SEQ ID NO 502: from 1 to 16
- Alignment No. 5354
- gi No. 4884866
- % Identity 70
- Alignment Length 180
- Location of Alignment in SEQ ID NO 502: from 1 to 28

- Alignment No. 5355
- gi No. 5081419
- % Identity 88.6
- Alignment Length 167
- Location of Alignment in SEQ ID NO 502: from 1 to 16
  
- Alignment No. 5356
- gi No. 5139543
- % Identity 74.3
- Alignment Length 180
- Location of Alignment in SEQ ID NO 502: from 1 to 28
  
- Alignment No. 5357
- gi No. 541950
- % Identity 73
- Alignment Length 180
- Location of Alignment in SEQ ID NO 502: from 1 to 28
  
- Alignment No. 5358
- gi No. 541951
- % Identity 73.9
- Alignment Length 180
- Location of Alignment in SEQ ID NO 502: from 1 to 28
  
- Alignment No. 5359
- gi No. 629784
- % Identity 71.1
- Alignment Length 166
- Location of Alignment in SEQ ID NO 502: from 1 to 16
  
- Alignment No. 5360
- gi No. 727411
- % Identity 81.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 502: from 15 to 147
  
- Alignment No. 5361
- gi No. 729503
- % Identity 80
- Alignment Length 140
- Location of Alignment in SEQ ID NO 502: from 15 to 154
  
- Alignment No. 5362
- gi No. 729504
- % Identity 78.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 502: from 15 to 154
  
- Alignment No. 5363
- gi No. 729505
- % Identity 82.1
- Alignment Length 145
- Location of Alignment in SEQ ID NO 502: from 15 to 154
  
- Alignment No. 5364
- gi No. 729506
- % Identity 93.6
- Alignment Length 140
- Location of Alignment in SEQ ID NO 502: from 15 to 154



- Alignment No. 5365
- gi No. 729507
- % Identity 81.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 502: from 15 to 154
  
- Alignment No. 5366
- gi No. 729508
- % Identity 83.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 502: from 15 to 154

Maximum Length Sequence corresponding to clone ID 120080

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 503
- Ceres seq\_id 1498550

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 504
- Ceres seq\_id 1498551
- Location of start within SEQ ID NO 503: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 505
- Ceres seq\_id 1498552
- Location of start within SEQ ID NO 503: at 117 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5367
- gi No. 4455186
- % Identity 97.7
- Alignment Length 88
- Location of Alignment in SEQ ID NO 505: from 1 to 87

Maximum Length Sequence corresponding to clone ID 120122

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 506
- Ceres seq\_id 1498553

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 507
- Ceres seq\_id 1498554
- Location of start within SEQ ID NO 506: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5368
- NAD dependent epimerase/dehydratase family
- Location within SEQ ID NO 507: from 29 to 362 aa.
  
- Alignment No. 5369
- 3-beta hydroxysteroid dehydrogenase/isomerase family
- Location within SEQ ID NO 507: from 24 to 235 aa.
  
- Alignment No. 5370
- 3-beta hydroxysteroid dehydrogenase/isomerase family
- Location within SEQ ID NO 507: from 230 to 322 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5371
- gi No. 1143533
- % Identity 73.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 507: from 28 to 61
  
- Alignment No. 5372
- gi No. 171547
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 507: from 29 to 62
  
- Alignment No. 5373
- gi No. 3021357
- % Identity 77.6
- Alignment Length 344
- Location of Alignment in SEQ ID NO 507: from 29 to 372
  
- Alignment No. 5374
- gi No. 3513739
- % Identity 80.2
- Alignment Length 344
- Location of Alignment in SEQ ID NO 507: from 25 to 368
  
- Alignment No. 5375
- gi No. 4539370
- % Identity 80.2
- Alignment Length 344
- Location of Alignment in SEQ ID NO 507: from 25 to 368
  
- Alignment No. 5376
- gi No. 4972096
- % Identity 79.6
- Alignment Length 348
- Location of Alignment in SEQ ID NO 507: from 25 to 372

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 508
- Ceres seq\_id 1498555
- Location of start within SEQ ID NO 506: at 73 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5377
- NAD dependent epimerase/dehydratase family
- Location within SEQ ID NO 508: from 5 to 338 aa.
  
- Alignment No. 5378
- 3-beta hydroxysteroid dehydrogenase/isomerase family
- Location within SEQ ID NO 508: from 1 to 211 aa.
  
- Alignment No. 5379
- 3-beta hydroxysteroid dehydrogenase/isomerase family
- Location within SEQ ID NO 508: from 206 to 298 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5380
- gi No. 1143533
- % Identity 73.5

- Alignment Length 34
- Location of Alignment in SEQ ID NO 508: from 4 to 37
- Alignment No. 5381
- gi No. 171547
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 508: from 5 to 38
- Alignment No. 5382
- gi No. 3021357
- % Identity 77.6
- Alignment Length 344
- Location of Alignment in SEQ ID NO 508: from 5 to 348
- Alignment No. 5383
- gi No. 3513739
- % Identity 80.2
- Alignment Length 344
- Location of Alignment in SEQ ID NO 508: from 1 to 344
- Alignment No. 5384
- gi No. 4539370
- % Identity 80.2
- Alignment Length 344
- Location of Alignment in SEQ ID NO 508: from 1 to 344
- Alignment No. 5385
- gi No. 4972096
- % Identity 79.6
- Alignment Length 348
- Location of Alignment in SEQ ID NO 508: from 1 to 348

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 509
- Ceres seq\_id 1498556
- Location of start within SEQ ID NO 506: at 319 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5386
- NAD dependent epimerase/dehydratase family
- Location within SEQ ID NO 509: from 1 to 256 aa.
- Alignment No. 5387
- 3-beta hydroxysteroid dehydrogenase/isomerase family
- Location within SEQ ID NO 509: from 1 to 129 aa.
- Alignment No. 5388
- 3-beta hydroxysteroid dehydrogenase/isomerase family
- Location within SEQ ID NO 509: from 124 to 216 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5389
- gi No. 3021357
- % Identity 77.6
- Alignment Length 344
- Location of Alignment in SEQ ID NO 509: from 1 to 266
- Alignment No. 5390
- gi No. 3513739

- % Identity 80.2
- Alignment Length 344
- Location of Alignment in SEQ ID NO 509: from 1 to 262
  
- Alignment No. 5391
- gi No. 4539370
- % Identity 80.2
- Alignment Length 344
- Location of Alignment in SEQ ID NO 509: from 1 to 262
  
- Alignment No. 5392
- gi No. 4972096
- % Identity 79.6
- Alignment Length 348
- Location of Alignment in SEQ ID NO 509: from 1 to 266

Maximum Length Sequence corresponding to clone ID 120302

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 510
- Ceres seq\_id 1498561

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 511
- Ceres seq\_id 1498562
- Location of start within SEQ ID NO 510: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5393
- gi No. 1200239
- % Identity 78.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 511: from 4 to 26
  
- Alignment No. 5394
- gi No. 1262382
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 511: from 2 to 23
  
- Alignment No. 5395
- gi No. 127585
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 511: from 2 to 27
  
- Alignment No. 5396
- gi No. 127586
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 511: from 2 to 27
  
- Alignment No. 5397
- gi No. 127588
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 511: from 2 to 28
  
- Alignment No. 5398
- gi No. 1491933
- % Identity 74.1

- Alignment Length 27
- Location of Alignment in SEQ ID NO 511: from 2 to 28
  
- Alignment No. 5399
- gi No. 1732513
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 511: from 2 to 27
  
- Alignment No. 5400
- gi No. 1946267
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 511: from 2 to 40
  
- Alignment No. 5401
- gi No. 2129563
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 511: from 2 to 40
  
- Alignment No. 5402
- gi No. 2129592
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 511: from 2 to 40
  
- Alignment No. 5403
- gi No. 2130045
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 511: from 2 to 28
  
- Alignment No. 5404
- gi No. 2130046
- % Identity 89.3
- Alignment Length 28
- Location of Alignment in SEQ ID NO 511: from 2 to 29
  
- Alignment No. 5405
- gi No. 2245137
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 511: from 2 to 40
  
- Alignment No. 5406
- gi No. 2343273
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 511: from 2 to 27
  
- Alignment No. 5407
- gi No. 2343275
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 511: from 2 to 27
  
- Alignment No. 5408
- gi No. 2529681
- % Identity 82.8
- Alignment Length 29

- Location of Alignment in SEQ ID NO 511: from 2 to 30
- Alignment No. 5409
- gi No. 2605617
- % Identity 82.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 511: from 2 to 41
- Alignment No. 5410
- gi No. 2605619
- % Identity 88.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 511: from 2 to 35
- Alignment No. 5411
- gi No. 2832408
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 511: from 2 to 31
- Alignment No. 5412
- gi No. 2921334
- % Identity 81.5
- Alignment Length 27
- Location of Alignment in SEQ ID NO 511: from 2 to 28
- Alignment No. 5413
- gi No. 2921336
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 511: from 2 to 28
- Alignment No. 5414
- gi No. 293900
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 511: from 2 to 27
- Alignment No. 5415
- gi No. 3080388
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 511: from 2 to 40
- Alignment No. 5416
- gi No. 309568
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 511: from 2 to 27
- Alignment No. 5417
- gi No. 309570
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 511: from 2 to 27
- Alignment No. 5418
- gi No. 309572
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 511: from 2 to 27

- Alignment No. 5419
- gi No. 3298534
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 511: from 4 to 27
  
- Alignment No. 5420
- gi No. 3941412
- % Identity 99.5
- Alignment Length 184
- Location of Alignment in SEQ ID NO 511: from 2 to 184
  
- Alignment No. 5421
- gi No. 3941414
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 511: from 2 to 40
  
- Alignment No. 5422
- gi No. 3941420
- % Identity 82.8
- Alignment Length 29
- Location of Alignment in SEQ ID NO 511: from 2 to 30
  
- Alignment No. 5423
- gi No. 3941434
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 511: from 2 to 27
  
- Alignment No. 5424
- gi No. 3941442
- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 511: from 4 to 27
  
- Alignment No. 5425
- gi No. 3941456
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 511: from 2 to 40
  
- Alignment No. 5426
- gi No. 3941490
- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 511: from 4 to 27
  
- Alignment No. 5427
- gi No. 3941500
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 511: from 2 to 27
  
- Alignment No. 5428
- gi No. 3941506
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 511: from 2 to 40

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- Alignment No. 5429
- gi No. 3941508
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 511: from 2 to 27
  
- Alignment No. 5430
- gi No. 3941512
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 511: from 2 to 27
  
- Alignment No. 5431
- gi No. 3941516
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 511: from 2 to 27
  
- Alignment No. 5432
- gi No. 3941522
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 511: from 2 to 27
  
- Alignment No. 5433
- gi No. 4467149
- % Identity 100
- Alignment Length 184
- Location of Alignment in SEQ ID NO 511: from 2 to 184
  
- Alignment No. 5434
- gi No. 4678374
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 511: from 2 to 27
  
- Alignment No. 5435
- gi No. 904102
- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 511: from 4 to 27

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 512
- Ceres seq\_id 1498563
- Location of start within SEQ ID NO 510: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5436
- gi No. 3941412
- % Identity 99.5
- Alignment Length 184
- Location of Alignment in SEQ ID NO 512: from 1 to 94
  
- Alignment No. 5437
- gi No. 4467149
- % Identity 100
- Alignment Length 184
- Location of Alignment in SEQ ID NO 512: from 1 to 94



Maximum Length Sequence corresponding to clone ID 120385

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 513
- Ceres seq\_id 1498564

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 514
- Ceres seq\_id 1498565
- Location of start within SEQ ID NO 513: at 46 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5438
- Elongation factor Tu family
- Location within SEQ ID NO 514: from 70 to 132 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5439
- gi No. 1169473
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
- Alignment No. 5440
- gi No. 1169475
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
- Alignment No. 5441
- gi No. 1169476
- % Identity 93.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
- Alignment No. 5442
- gi No. 119132
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
- Alignment No. 5443
- gi No. 119138
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
- Alignment No. 5444
- gi No. 119140
- % Identity 73.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
- Alignment No. 5445
- gi No. 119143
- % Identity 95.6
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
- Alignment No. 5446
- gi No. 119146

- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5447
- gi No. 119150
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5448
- gi No. 119161
- % Identity 73.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5449
- gi No. 1220311
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 514: from 98 to 141
  
- Alignment No. 5450
- gi No. 1220484
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5451
- gi No. 1235563
- % Identity 86.7
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5452
- gi No. 1352345
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5453
- gi No. 168386
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 514: from 131 to 142
  
- Alignment No. 5454
- gi No. 1732359
- % Identity 93.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5455
- gi No. 181967
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5456
- gi No. 1864017
- % Identity 93.3

- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5457
- gi No. 203992
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5458
- gi No. 206440
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 514: from 98 to 141
  
- Alignment No. 5459
- gi No. 2130149
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5460
- gi No. 214113
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5461
- gi No. 2282584
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5462
- gi No. 2293575
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5463
- gi No. 232029
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5464
- gi No. 262525
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 514: from 119 to 137
  
- Alignment No. 5465
- gi No. 2662341
- % Identity 91.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5466
- gi No. 2662343
- % Identity 91.1
- Alignment Length 45

- Location of Alignment in SEQ ID NO 514: from 98 to 142
- Alignment No. 5467
- gi No. 2791834
- % Identity 86.7
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
- Alignment No. 5468
- gi No. 2996096
- % Identity 91.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
- Alignment No. 5469
- gi No. 31092
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
- Alignment No. 5470
- gi No. 3122053
- % Identity 91.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
- Alignment No. 5471
- gi No. 3122060
- % Identity 91.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
- Alignment No. 5472
- gi No. 3122071
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
- Alignment No. 5473
- gi No. 3122072
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
- Alignment No. 5474
- gi No. 3158376
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 514: from 1 to 109
- Alignment No. 5475
- gi No. 3319882
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
- Alignment No. 5476
- gi No. 3413167
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142

- Alignment No. 5477
- gi No. 3869088
- % Identity 91.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5478
- gi No. 3869142
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5479
- gi No. 399414
- % Identity 80
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5480
- gi No. 4138179
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5481
- gi No. 4503471
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5482
- gi No. 461987
- % Identity 84.4
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5483
- gi No. 461988
- % Identity 80
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5484
- gi No. 4680249
- % Identity 91.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5485
- gi No. 542125
- % Identity 80
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5486
- gi No. 5670158
- % Identity 75.6
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142

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- Alignment No. 5487
- gi No. 64659
- % Identity 73.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5488
- gi No. 65104
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5489
- gi No. 72870
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5490
- gi No. 99688
- % Identity 95.6
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142
  
- Alignment No. 5491
- gi No. 99902
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 514: from 98 to 142

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 515
- Ceres seq\_id 1498566
- Location of start within SEQ ID NO 513: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5492
- Elongation factor Tu family
- Location within SEQ ID NO 515: from 22 to 84 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5493
- gi No. 1169473
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5494
- gi No. 1169475
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5495
- gi No. 1169476
- % Identity 93.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5496

- gi No. 119132
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5497
- gi No. 119138
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5498
- gi No. 119140
- % Identity 73.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5499
- gi No. 119143
- % Identity 95.6
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5500
- gi No. 119146
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5501
- gi No. 119150
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5502
- gi No. 119161
- % Identity 73.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5503
- gi No. 1220311
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 515: from 50 to 93
  
- Alignment No. 5504
- gi No. 1220484
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5505
- gi No. 1235563
- % Identity 86.7
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5506
- gi No. 1352345

- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5507
- gi No. 168386
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 515: from 83 to 94
  
- Alignment No. 5508
- gi No. 1732359
- % Identity 93.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5509
- gi No. 181967
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5510
- gi No. 1864017
- % Identity 93.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5511
- gi No. 203992
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5512
- gi No. 206440
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 515: from 50 to 93
  
- Alignment No. 5513
- gi No. 2130149
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5514
- gi No. 214113
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5515
- gi No. 2282584
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5516
- gi No. 2293575
- % Identity 71.1



- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5517
- gi No. 232029
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5518
- gi No. 262525
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 515: from 71 to 89
  
- Alignment No. 5519
- gi No. 2662341
- % Identity 91.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5520
- gi No. 2662343
- % Identity 91.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5521
- gi No. 2791834
- % Identity 86.7
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5522
- gi No. 2996096
- % Identity 91.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5523
- gi No. 31092
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5524
- gi No. 3122053
- % Identity 91.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5525
- gi No. 3122060
- % Identity 91.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5526
- gi No. 3122071
- % Identity 88.9
- Alignment Length 45

- Location of Alignment in SEQ ID NO 515: from 50 to 94
- Alignment No. 5527
- gi No. 3122072
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
- Alignment No. 5528
- gi No. 3158376
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 515: from 1 to 61
- Alignment No. 5529
- gi No. 3319882
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
- Alignment No. 5530
- gi No. 3413167
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
- Alignment No. 5531
- gi No. 3869088
- % Identity 91.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
- Alignment No. 5532
- gi No. 3869142
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
- Alignment No. 5533
- gi No. 399414
- % Identity 80
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
- Alignment No. 5534
- gi No. 4138179
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
- Alignment No. 5535
- gi No. 4503471
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
- Alignment No. 5536
- gi No. 461987
- % Identity 84.4
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94

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- Alignment No. 5537
- gi No. 461988
- % Identity 80
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5538
- gi No. 4680249
- % Identity 91.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5539
- gi No. 542125
- % Identity 80
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5540
- gi No. 5670158
- % Identity 75.6
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5541
- gi No. 64659
- % Identity 73.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5542
- gi No. 65104
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5543
- gi No. 72870
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5544
- gi No. 99688
- % Identity 95.6
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94
  
- Alignment No. 5545
- gi No. 99902
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 515: from 50 to 94

Maximum Length Sequence corresponding to clone ID 121006

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 516
- Ceres seq\_id 1498567

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 517

- Ceres seq\_id 1498568
- Location of start within SEQ ID NO 516: at 85 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5546
- gi No. 118575
- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 517: from 1 to 44
  
- Alignment No. 5547
- gi No. 1592670
- % Identity 100
- Alignment Length 44
- Location of Alignment in SEQ ID NO 517: from 1 to 44
  
- Alignment No. 5548
- gi No. 1706562
- % Identity 70.7
- Alignment Length 41
- Location of Alignment in SEQ ID NO 517: from 1 to 41

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 518
- Ceres seq\_id 1498569
- Location of start within SEQ ID NO 516: at 378 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 121432

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 519
- Ceres seq\_id 1498574

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 520
- Ceres seq\_id 1498575
- Location of start within SEQ ID NO 519: at 121 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5549
- gi No. 2660671
- % Identity 99.5
- Alignment Length 375
- Location of Alignment in SEQ ID NO 520: from 1 to 375

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 521
- Ceres seq\_id 1498576
- Location of start within SEQ ID NO 519: at 628 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5550
- gi No. 2660671

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- % Identity 99.5
- Alignment Length 375
- Location of Alignment in SEQ ID NO 521: from 1 to 206

Maximum Length Sequence corresponding to clone ID 121628

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 522
- Ceres seq\_id 1498577

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 523
- Ceres seq\_id 1498578
- Location of start within SEQ ID NO 522: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5551
- gi No. 3064173
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 523: from 24 to 45
  
- Alignment No. 5552
- gi No. 643438
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 523: from 24 to 45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 524
- Ceres seq\_id 1498579
- Location of start within SEQ ID NO 522: at 47 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5553
- gi No. 3064173
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 524: from 9 to 30
  
- Alignment No. 5554
- gi No. 643438
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 524: from 9 to 30

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 525
- Ceres seq\_id 1498580
- Location of start within SEQ ID NO 522: at 50 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5555
- gi No. 3064173
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 525: from 8 to 29

- Alignment No. 5556
- gi No. 643438
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 525: from 8 to 29

Maximum Length Sequence corresponding to clone ID 123030

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 526
- Ceres seq\_id 1498593

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 527
- Ceres seq\_id 1498594
- Location of start within SEQ ID NO 526: at 124 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5557
- gi No. 2809244
- % Identity 92.2
- Alignment Length 313
- Location of Alignment in SEQ ID NO 527: from 1 to 308
  
- Alignment No. 5558
- gi No. 4206196
- % Identity 83.2
- Alignment Length 305
- Location of Alignment in SEQ ID NO 527: from 9 to 303

Maximum Length Sequence corresponding to clone ID 123244

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 528
- Ceres seq\_id 1498595

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 529
- Ceres seq\_id 1498596
- Location of start within SEQ ID NO 528: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5559
- gi No. 2781353
- % Identity 87.4
- Alignment Length 119
- Location of Alignment in SEQ ID NO 529: from 5 to 122

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 530
- Ceres seq\_id 1498597
- Location of start within SEQ ID NO 528: at 13 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5560
- gi No. 2781353
- % Identity 87.4
- Alignment Length 119

- Location of Alignment in SEQ ID NO 530: from 1 to 118

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 531
- Ceres seq\_id 1498598
- Location of start within SEQ ID NO 528: at 73 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5561
- gi No. 2781353
- % Identity 87.4
- Alignment Length 119
- Location of Alignment in SEQ ID NO 531: from 1 to 98

Maximum Length Sequence corresponding to clone ID 123547

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 532
- Ceres seq\_id 1498599

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 533
- Ceres seq\_id 1498600
- Location of start within SEQ ID NO 532: at 743 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5562
- Multicopper oxidase
- Location within SEQ ID NO 533: from 186 to 288 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5563
- gi No. 114268
- % Identity 74.2
- Alignment Length 550
- Location of Alignment in SEQ ID NO 533: from 1 to 339
- Alignment No. 5564
- gi No. 4204257
- % Identity 75.9
- Alignment Length 547
- Location of Alignment in SEQ ID NO 533: from 1 to 335
- Alignment No. 5565
- gi No. 4204258
- % Identity 93.2
- Alignment Length 561
- Location of Alignment in SEQ ID NO 533: from 1 to 341
- Alignment No. 5566
- gi No. 99807
- % Identity 74.9
- Alignment Length 550
- Location of Alignment in SEQ ID NO 533: from 1 to 339
- Alignment No. 5567
- gi No. 99808
- % Identity 73.3
- Alignment Length 550
- Location of Alignment in SEQ ID NO 533: from 1 to 339

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- Alignment No. 5568
- gi No. 99809
- % Identity 74
- Alignment Length 550
- Location of Alignment in SEQ ID NO 533: from 1 to 339

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 534
- Ceres seq\_id 1498601
- Location of start within SEQ ID NO 532: at 827 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5569
- Multicopper oxidase
- Location within SEQ ID NO 534: from 158 to 260 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5570
- gi No. 114268
- % Identity 74.2
- Alignment Length 550
- Location of Alignment in SEQ ID NO 534: from 1 to 311
  
- Alignment No. 5571
- gi No. 4204257
- % Identity 75.9
- Alignment Length 547
- Location of Alignment in SEQ ID NO 534: from 1 to 307
  
- Alignment No. 5572
- gi No. 4204258
- % Identity 93.2
- Alignment Length 561
- Location of Alignment in SEQ ID NO 534: from 1 to 313
  
- Alignment No. 5573
- gi No. 99807
- % Identity 74.9
- Alignment Length 550
- Location of Alignment in SEQ ID NO 534: from 1 to 311
  
- Alignment No. 5574
- gi No. 99808
- % Identity 73.3
- Alignment Length 550
- Location of Alignment in SEQ ID NO 534: from 1 to 311
  
- Alignment No. 5575
- gi No. 99809
- % Identity 74
- Alignment Length 550
- Location of Alignment in SEQ ID NO 534: from 1 to 311

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 535
- Ceres seq\_id 1498602
- Location of start within SEQ ID NO 532: at 842 nt.



(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5576
- Multicopper oxidase
- Location within SEQ ID NO 535: from 153 to 255 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5577
- gi No. 114268
- % Identity 74.2
- Alignment Length 550
- Location of Alignment in SEQ ID NO 535: from 1 to 306
- Alignment No. 5578
- gi No. 4204257
- % Identity 75.9
- Alignment Length 547
- Location of Alignment in SEQ ID NO 535: from 1 to 302
- Alignment No. 5579
- gi No. 4204258
- % Identity 93.2
- Alignment Length 561
- Location of Alignment in SEQ ID NO 535: from 1 to 308
- Alignment No. 5580
- gi No. 99807
- % Identity 74.9
- Alignment Length 550
- Location of Alignment in SEQ ID NO 535: from 1 to 306
- Alignment No. 5581
- gi No. 99808
- % Identity 73.3
- Alignment Length 550
- Location of Alignment in SEQ ID NO 535: from 1 to 306
- Alignment No. 5582
- gi No. 99809
- % Identity 74
- Alignment Length 550
- Location of Alignment in SEQ ID NO 535: from 1 to 306

Maximum Length Sequence corresponding to clone ID 124372

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 536
- Ceres seq\_id 1498610

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 537
- Ceres seq\_id 1498611
- Location of start within SEQ ID NO 536: at 453 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5583
- Glutamine synthetase
- Location within SEQ ID NO 537: from 1 to 254 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5584
- gi No. 100878

- % Identity 77.4
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5585
- gi No. 1076473
- % Identity 83.2
- Alignment Length 280
- Location of Alignment in SEQ ID NO 537: from 1 to 263
  
- Alignment No. 5586
- gi No. 1076474
- % Identity 92.6
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5587
- gi No. 1076475
- % Identity 95.4
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5588
- gi No. 1076487
- % Identity 83.5
- Alignment Length 279
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5589
- gi No. 1084350
- % Identity 94.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5590
- gi No. 1084412
- % Identity 73.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5591
- gi No. 1169926
- % Identity 86.8
- Alignment Length 281
- Location of Alignment in SEQ ID NO 537: from 1 to 264
  
- Alignment No. 5592
- gi No. 1169931
- % Identity 89.7
- Alignment Length 282
- Location of Alignment in SEQ ID NO 537: from 1 to 265
  
- Alignment No. 5593
- gi No. 121332
- % Identity 86.5
- Alignment Length 281
- Location of Alignment in SEQ ID NO 537: from 1 to 264
  
- Alignment No. 5594
- gi No. 121333
- % Identity 88.6

- Alignment Length 281
- Location of Alignment in SEQ ID NO 537: from 1 to 264
- Alignment No. 5595
- gi No. 121334
- % Identity 88
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5596
- gi No. 121336
- % Identity 88.9
- Alignment Length 279
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5597
- gi No. 121340
- % Identity 76.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5598
- gi No. 121341
- % Identity 77.4
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5599
- gi No. 121343
- % Identity 78.4
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5600
- gi No. 121344
- % Identity 79.5
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5601
- gi No. 121345
- % Identity 87.3
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5602
- gi No. 121348
- % Identity 83.5
- Alignment Length 242
- Location of Alignment in SEQ ID NO 537: from 1 to 225
- Alignment No. 5603
- gi No. 121349
- % Identity 87.6
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5604
- gi No. 121350
- % Identity 86.9
- Alignment Length 283

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- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5605
- gi No. 121351
- % Identity 88.3
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5606
- gi No. 121353
- % Identity 81.3
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5607
- gi No. 121368
- % Identity 89
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5608
- gi No. 121373
- % Identity 87.9
- Alignment Length 280
- Location of Alignment in SEQ ID NO 537: from 1 to 263
- Alignment No. 5609
- gi No. 1246768
- % Identity 90.1
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5610
- gi No. 1419092
- % Identity 85.9
- Alignment Length 277
- Location of Alignment in SEQ ID NO 537: from 1 to 260
- Alignment No. 5611
- gi No. 1419094
- % Identity 88
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5612
- gi No. 1527223
- % Identity 97.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 537: from 174 to 244
- Alignment No. 5613
- gi No. 169343
- % Identity 87.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 537: from 126 to 266
- Alignment No. 5614
- gi No. 1707955
- % Identity 88.3
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266

- Alignment No. 5615
- gi No. 1707959
- % Identity 90.1
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5616
- gi No. 1707962
- % Identity 87.5
- Alignment Length 280
- Location of Alignment in SEQ ID NO 537: from 1 to 263
  
- Alignment No. 5617
- gi No. 1707963
- % Identity 82
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5618
- gi No. 1835154
- % Identity 89
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5619
- gi No. 1835156
- % Identity 89
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5620
- gi No. 1934754
- % Identity 77.4
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5621
- gi No. 1934756
- % Identity 92.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5622
- gi No. 1934758
- % Identity 92.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5623
- gi No. 2073448
- % Identity 90.5
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5624
- gi No. 2118353
- % Identity 87.2
- Alignment Length 242
- Location of Alignment in SEQ ID NO 537: from 23 to 264

- Alignment No. 5625
- gi No. 2129882
- % Identity 85.5
- Alignment Length 276
- Location of Alignment in SEQ ID NO 537: from 1 to 264
  
- Alignment No. 5626
- gi No. 2129883
- % Identity 88.3
- Alignment Length 281
- Location of Alignment in SEQ ID NO 537: from 1 to 264
  
- Alignment No. 5627
- gi No. 2197152
- % Identity 90.6
- Alignment Length 159
- Location of Alignment in SEQ ID NO 537: from 109 to 266
  
- Alignment No. 5628
- gi No. 2197154
- % Identity 77.1
- Alignment Length 157
- Location of Alignment in SEQ ID NO 537: from 110 to 266
  
- Alignment No. 5629
- gi No. 2197156
- % Identity 73.7
- Alignment Length 156
- Location of Alignment in SEQ ID NO 537: from 111 to 266
  
- Alignment No. 5630
- gi No. 2197158
- % Identity 75.8
- Alignment Length 157
- Location of Alignment in SEQ ID NO 537: from 110 to 266
  
- Alignment No. 5631
- gi No. 2209145
- % Identity 90.9
- Alignment Length 154
- Location of Alignment in SEQ ID NO 537: from 109 to 262
  
- Alignment No. 5632
- gi No. 2209147
- % Identity 83.9
- Alignment Length 155
- Location of Alignment in SEQ ID NO 537: from 109 to 263
  
- Alignment No. 5633
- gi No. 2209149
- % Identity 91.6
- Alignment Length 155
- Location of Alignment in SEQ ID NO 537: from 109 to 263
  
- Alignment No. 5634
- gi No. 2213877
- % Identity 91.2
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5635

- gi No. 226547
- % Identity 80.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5636
- gi No. 228454
- % Identity 98.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5637
- gi No. 228455
- % Identity 92.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5638
- gi No. 228456
- % Identity 84.8
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5639
- gi No. 2454629
- % Identity 86.1
- Alignment Length 280
- Location of Alignment in SEQ ID NO 537: from 1 to 263
  
- Alignment No. 5640
- gi No. 2454631
- % Identity 87.3
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5641
- gi No. 2454633
- % Identity 78.8
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5642
- gi No. 2811030
- % Identity 88.5
- Alignment Length 279
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5643
- gi No. 286122
- % Identity 86.6
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5644
- gi No. 286124
- % Identity 86.2
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5645
- gi No. 3023870

- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 537: from 48 to 62
  
- Alignment No. 5646
- gi No. 312276
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 537: from 244 to 264
  
- Alignment No. 5647
- gi No. 312301
- % Identity 87
- Alignment Length 23
- Location of Alignment in SEQ ID NO 537: from 244 to 266
  
- Alignment No. 5648
- gi No. 322646
- % Identity 77.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5649
- gi No. 322833
- % Identity 82.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5650
- gi No. 3695295
- % Identity 86.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5651
- gi No. 396547
- % Identity 82
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5652
- gi No. 4138351
- % Identity 84.5
- Alignment Length 277
- Location of Alignment in SEQ ID NO 537: from 1 to 260
  
- Alignment No. 5653
- gi No. 4138395
- % Identity 77.8
- Alignment Length 126
- Location of Alignment in SEQ ID NO 537: from 1 to 109
  
- Alignment No. 5654
- gi No. 417060
- % Identity 88.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5655
- gi No. 4650846
- % Identity 90.9

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- Alignment Length 55
- Location of Alignment in SEQ ID NO 537: from 183 to 237
  
- Alignment No. 5656
- gi No. 4731322
- % Identity 80.2
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5657
- gi No. 4731357
- % Identity 83.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 537: from 1 to 96
  
- Alignment No. 5658
- gi No. 481914
- % Identity 92.6
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5659
- gi No. 487042
- % Identity 86.7
- Alignment Length 158
- Location of Alignment in SEQ ID NO 537: from 109 to 266
  
- Alignment No. 5660
- gi No. 4884970
- % Identity 79.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5661
- gi No. 4884972
- % Identity 86.2
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5662
- gi No. 5326657
- % Identity 80.7
- Alignment Length 88
- Location of Alignment in SEQ ID NO 537: from 93 to 180
  
- Alignment No. 5663
- gi No. 5326659
- % Identity 79.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 537: from 90 to 185
  
- Alignment No. 5664
- gi No. 5326666
- % Identity 78.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 537: from 90 to 185
  
- Alignment No. 5665
- gi No. 541632
- % Identity 89
- Alignment Length 172

- Location of Alignment in SEQ ID NO 537: from 92 to 263
- Alignment No. 5666
- gi No. 541962
- % Identity 88
- Alignment Length 50
- Location of Alignment in SEQ ID NO 537: from 217 to 266
- Alignment No. 5667
- gi No. 541963
- % Identity 90
- Alignment Length 50
- Location of Alignment in SEQ ID NO 537: from 217 to 266
- Alignment No. 5668
- gi No. 553034
- % Identity 86.8
- Alignment Length 91
- Location of Alignment in SEQ ID NO 537: from 176 to 266
- Alignment No. 5669
- gi No. 555970
- % Identity 78.3
- Alignment Length 175
- Location of Alignment in SEQ ID NO 537: from 92 to 266
- Alignment No. 5670
- gi No. 561674
- % Identity 88.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5671
- gi No. 5701896
- % Identity 76
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5672
- gi No. 585201
- % Identity 88.3
- Alignment Length 282
- Location of Alignment in SEQ ID NO 537: from 1 to 265
- Alignment No. 5673
- gi No. 585202
- % Identity 81.1
- Alignment Length 286
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5674
- gi No. 585203
- % Identity 85.5
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5675
- gi No. 585204
- % Identity 85.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266

- Alignment No. 5676
- gi No. 587120
- % Identity 82.4
- Alignment Length 279
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5677
- gi No. 68589
- % Identity 89
- Alignment Length 282
- Location of Alignment in SEQ ID NO 537: from 1 to 265
- Alignment No. 5678
- gi No. 68592
- % Identity 87.6
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5679
- gi No. 68599
- % Identity 76.3
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5680
- gi No. 699621
- % Identity 86.8
- Alignment Length 281
- Location of Alignment in SEQ ID NO 537: from 1 to 264
- Alignment No. 5681
- gi No. 699623
- % Identity 88.3
- Alignment Length 282
- Location of Alignment in SEQ ID NO 537: from 1 to 265
- Alignment No. 5682
- gi No. 729590
- % Identity 82.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5683
- gi No. 755762
- % Identity 76.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5684
- gi No. 829285
- % Identity 79.5
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
- Alignment No. 5685
- gi No. 829286
- % Identity 86.5
- Alignment Length 259
- Location of Alignment in SEQ ID NO 537: from 8 to 266

- Alignment No. 5686
- gi No. 99696
- % Identity 77.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5687
- gi No. 99697
- % Identity 92.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5688
- gi No. 99698
- % Identity 84.8
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266
  
- Alignment No. 5689
- gi No. 99699
- % Identity 98.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 537: from 1 to 266

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 538
- Ceres seq\_id 1498612
- Location of start within SEQ ID NO 536: at 762 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5690
- Glutamine synthetase
- Location within SEQ ID NO 538: from 1 to 151 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5691
- gi No. 100878
- % Identity 77.4
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5692
- gi No. 1076473
- % Identity 83.2
- Alignment Length 280
- Location of Alignment in SEQ ID NO 538: from 1 to 160
  
- Alignment No. 5693
- gi No. 1076474
- % Identity 92.6
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5694
- gi No. 1076475
- % Identity 95.4
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5695

- gi No. 1076487
- % Identity 83.5
- Alignment Length 279
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5696
- gi No. 1084350
- % Identity 94.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5697
- gi No. 1084412
- % Identity 73.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5698
- gi No. 1169926
- % Identity 86.8
- Alignment Length 281
- Location of Alignment in SEQ ID NO 538: from 1 to 161
  
- Alignment No. 5699
- gi No. 1169931
- % Identity 89.7
- Alignment Length 282
- Location of Alignment in SEQ ID NO 538: from 1 to 162
  
- Alignment No. 5700
- gi No. 121332
- % Identity 86.5
- Alignment Length 281
- Location of Alignment in SEQ ID NO 538: from 1 to 161
  
- Alignment No. 5701
- gi No. 121333
- % Identity 88.6
- Alignment Length 281
- Location of Alignment in SEQ ID NO 538: from 1 to 161
  
- Alignment No. 5702
- gi No. 121334
- % Identity 88
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5703
- gi No. 121336
- % Identity 88.9
- Alignment Length 279
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5704
- gi No. 121340
- % Identity 76.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5705
- gi No. 121341

- % Identity 77.4
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5706
- gi No. 121343
- % Identity 78.4
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5707
- gi No. 121344
- % Identity 79.5
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5708
- gi No. 121345
- % Identity 87.3
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5709
- gi No. 121348
- % Identity 83.5
- Alignment Length 242
- Location of Alignment in SEQ ID NO 538: from 1 to 122
  
- Alignment No. 5710
- gi No. 121349
- % Identity 87.6
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5711
- gi No. 121350
- % Identity 86.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5712
- gi No. 121351
- % Identity 88.3
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5713
- gi No. 121353
- % Identity 81.3
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5714
- gi No. 121368
- % Identity 89
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5715
- gi No. 121373
- % Identity 87.9

- Alignment Length 280
- Location of Alignment in SEQ ID NO 538: from 1 to 160
- Alignment No. 5716
- gi No. 1246768
- % Identity 90.1
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5717
- gi No. 1419092
- % Identity 85.9
- Alignment Length 277
- Location of Alignment in SEQ ID NO 538: from 1 to 157
- Alignment No. 5718
- gi No. 1419094
- % Identity 88
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5719
- gi No. 1527223
- % Identity 97.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 538: from 71 to 141
- Alignment No. 5720
- gi No. 169343
- % Identity 87.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 538: from 23 to 163
- Alignment No. 5721
- gi No. 1707955
- % Identity 88.3
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5722
- gi No. 1707959
- % Identity 90.1
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5723
- gi No. 1707962
- % Identity 87.5
- Alignment Length 280
- Location of Alignment in SEQ ID NO 538: from 1 to 160
- Alignment No. 5724
- gi No. 1707963
- % Identity 82
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5725
- gi No. 1835154
- % Identity 89
- Alignment Length 283

- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5726
- gi No. 1835156
- % Identity 89
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5727
- gi No. 1934754
- % Identity 77.4
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5728
- gi No. 1934756
- % Identity 92.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5729
- gi No. 1934758
- % Identity 92.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5730
- gi No. 2073448
- % Identity 90.5
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5731
- gi No. 2118353
- % Identity 87.2
- Alignment Length 242
- Location of Alignment in SEQ ID NO 538: from 1 to 161
- Alignment No. 5732
- gi No. 2129882
- % Identity 85.5
- Alignment Length 276
- Location of Alignment in SEQ ID NO 538: from 1 to 161
- Alignment No. 5733
- gi No. 2129883
- % Identity 88.3
- Alignment Length 281
- Location of Alignment in SEQ ID NO 538: from 1 to 161
- Alignment No. 5734
- gi No. 2197152
- % Identity 90.6
- Alignment Length 159
- Location of Alignment in SEQ ID NO 538: from 6 to 163
- Alignment No. 5735
- gi No. 2197154
- % Identity 77.1
- Alignment Length 157
- Location of Alignment in SEQ ID NO 538: from 7 to 163



- Alignment No. 5736
- gi No. 2197156
- % Identity 73.7
- Alignment Length 156
- Location of Alignment in SEQ ID NO 538: from 8 to 163
  
- Alignment No. 5737
- gi No. 2197158
- % Identity 75.8
- Alignment Length 157
- Location of Alignment in SEQ ID NO 538: from 7 to 163
  
- Alignment No. 5738
- gi No. 2209145
- % Identity 90.9
- Alignment Length 154
- Location of Alignment in SEQ ID NO 538: from 6 to 159
  
- Alignment No. 5739
- gi No. 2209147
- % Identity 83.9
- Alignment Length 155
- Location of Alignment in SEQ ID NO 538: from 6 to 160
  
- Alignment No. 5740
- gi No. 2209149
- % Identity 91.6
- Alignment Length 155
- Location of Alignment in SEQ ID NO 538: from 6 to 160
  
- Alignment No. 5741
- gi No. 2213877
- % Identity 91.2
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5742
- gi No. 226547
- % Identity 80.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5743
- gi No. 228454
- % Identity 98.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5744
- gi No. 228455
- % Identity 92.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5745
- gi No. 228456
- % Identity 84.8
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163

- Alignment No. 5746
- gi No. 2454629
- % Identity 86.1
- Alignment Length 280
- Location of Alignment in SEQ ID NO 538: from 1 to 160
  
- Alignment No. 5747
- gi No. 2454631
- % Identity 87.3
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5748
- gi No. 2454633
- % Identity 78.8
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5749
- gi No. 2811030
- % Identity 88.5
- Alignment Length 279
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5750
- gi No. 286122
- % Identity 86.6
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5751
- gi No. 286124
- % Identity 86.2
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5752
- gi No. 312276
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 538: from 141 to 161
  
- Alignment No. 5753
- gi No. 312301
- % Identity 87
- Alignment Length 23
- Location of Alignment in SEQ ID NO 538: from 141 to 163
  
- Alignment No. 5754
- gi No. 322646
- % Identity 77.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5755
- gi No. 322833
- % Identity 82.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5756

- gi No. 3695295
- % Identity 86.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5757
- gi No. 396547
- % Identity 82
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5758
- gi No. 4138351
- % Identity 84.5
- Alignment Length 277
- Location of Alignment in SEQ ID NO 538: from 1 to 157
  
- Alignment No. 5759
- gi No. 417060
- % Identity 88.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5760
- gi No. 4650846
- % Identity 90.9
- Alignment Length 55
- Location of Alignment in SEQ ID NO 538: from 80 to 134
  
- Alignment No. 5761
- gi No. 4731322
- % Identity 80.2
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5762
- gi No. 481914
- % Identity 92.6
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5763
- gi No. 487042
- % Identity 86.7
- Alignment Length 158
- Location of Alignment in SEQ ID NO 538: from 6 to 163
  
- Alignment No. 5764
- gi No. 4884970
- % Identity 79.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5765
- gi No. 4884972
- % Identity 86.2
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5766
- gi No. 5326657

- % Identity 80.7
- Alignment Length 88
- Location of Alignment in SEQ ID NO 538: from 1 to 77
  
- Alignment No. 5767
- gi No. 5326659
- % Identity 79.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 538: from 1 to 82
  
- Alignment No. 5768
- gi No. 5326666
- % Identity 78.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 538: from 1 to 82
  
- Alignment No. 5769
- gi No. 541632
- % Identity 89
- Alignment Length 172
- Location of Alignment in SEQ ID NO 538: from 1 to 160
  
- Alignment No. 5770
- gi No. 541962
- % Identity 88
- Alignment Length 50
- Location of Alignment in SEQ ID NO 538: from 114 to 163
  
- Alignment No. 5771
- gi No. 541963
- % Identity 90
- Alignment Length 50
- Location of Alignment in SEQ ID NO 538: from 114 to 163
  
- Alignment No. 5772
- gi No. 553034
- % Identity 86.8
- Alignment Length 91
- Location of Alignment in SEQ ID NO 538: from 73 to 163
  
- Alignment No. 5773
- gi No. 555970
- % Identity 78.3
- Alignment Length 175
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5774
- gi No. 561674
- % Identity 88.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5775
- gi No. 5701896
- % Identity 76
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5776
- gi No. 585201
- % Identity 88.3

- Alignment Length 282
- Location of Alignment in SEQ ID NO 538: from 1 to 162
  
- Alignment No. 5777
- gi No. 585202
- % Identity 81.1
- Alignment Length 286
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5778
- gi No. 585203
- % Identity 85.5
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5779
- gi No. 585204
- % Identity 85.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5780
- gi No. 587120
- % Identity 82.4
- Alignment Length 279
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5781
- gi No. 68589
- % Identity 89
- Alignment Length 282
- Location of Alignment in SEQ ID NO 538: from 1 to 162
  
- Alignment No. 5782
- gi No. 68592
- % Identity 87.6
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5783
- gi No. 68599
- % Identity 76.3
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
  
- Alignment No. 5784
- gi No. 699621
- % Identity 86.8
- Alignment Length 281
- Location of Alignment in SEQ ID NO 538: from 1 to 161
  
- Alignment No. 5785
- gi No. 699623
- % Identity 88.3
- Alignment Length 282
- Location of Alignment in SEQ ID NO 538: from 1 to 162
  
- Alignment No. 5786
- gi No. 729590
- % Identity 82.7
- Alignment Length 283

- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5787
- gi No. 755762
- % Identity 76.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5788
- gi No. 829285
- % Identity 79.5
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5789
- gi No. 829286
- % Identity 86.5
- Alignment Length 259
- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5790
- gi No. 99696
- % Identity 77.7
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5791
- gi No. 99697
- % Identity 92.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5792
- gi No. 99698
- % Identity 84.8
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163
- Alignment No. 5793
- gi No. 99699
- % Identity 98.9
- Alignment Length 283
- Location of Alignment in SEQ ID NO 538: from 1 to 163

Maximum Length Sequence corresponding to clone ID 125153

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 539
- Ceres seq\_id 1498616

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 540
- Ceres seq\_id 1498617
- Location of start within SEQ ID NO 539: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5794
- Diacylglycerol kinase catalytic domain (presumed)
- Location within SEQ ID NO 540: from 79 to 220 aa.
- Alignment No. 5795
- Diacylglycerol kinase accessory domain (presumed)

- Location within SEQ ID NO 540: from 273 to 431 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5796
- gi No. 4454484
- % Identity 97.6
- Alignment Length 499
- Location of Alignment in SEQ ID NO 540: from 40 to 530
- Alignment No. 5797
- gi No. 4455371
- % Identity 73.3
- Alignment Length 221
- Location of Alignment in SEQ ID NO 540: from 40 to 260

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 541
- Ceres seq\_id 1498618
- Location of start within SEQ ID NO 539: at 119 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5798
- Diacylglycerol kinase catalytic domain (presumed)
- Location within SEQ ID NO 541: from 40 to 181 aa.
- Alignment No. 5799
- Diacylglycerol kinase accessory domain (presumed)
- Location within SEQ ID NO 541: from 234 to 392 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5800
- gi No. 4454484
- % Identity 97.6
- Alignment Length 499
- Location of Alignment in SEQ ID NO 541: from 1 to 491
- Alignment No. 5801
- gi No. 4455371
- % Identity 73.3
- Alignment Length 221
- Location of Alignment in SEQ ID NO 541: from 1 to 221

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 542
- Ceres seq\_id 1498619
- Location of start within SEQ ID NO 539: at 644 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5802
- Diacylglycerol kinase accessory domain (presumed)
- Location within SEQ ID NO 542: from 59 to 217 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5803
- gi No. 4454484
- % Identity 97.6
- Alignment Length 499
- Location of Alignment in SEQ ID NO 542: from 1 to 316

- Alignment No. 5804
- gi No. 4455371
- % Identity 73.3
- Alignment Length 221
- Location of Alignment in SEQ ID NO 542: from 1 to 46

Maximum Length Sequence corresponding to clone ID 125863

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 543
- Ceres seq\_id 1498628

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 544
- Ceres seq\_id 1498629
- Location of start within SEQ ID NO 543: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5805
- gi No. 4741923
- % Identity 98.6
- Alignment Length 218
- Location of Alignment in SEQ ID NO 544: from 29 to 246

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 545
- Ceres seq\_id 1498630
- Location of start within SEQ ID NO 543: at 86 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5806
- gi No. 4741923
- % Identity 98.6
- Alignment Length 218
- Location of Alignment in SEQ ID NO 545: from 1 to 218

Maximum Length Sequence corresponding to clone ID 125981

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 546
- Ceres seq\_id 1498631

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 547
- Ceres seq\_id 1498632
- Location of start within SEQ ID NO 546: at 61 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5807
- gi No. 4455180
- % Identity 92.8
- Alignment Length 432
- Location of Alignment in SEQ ID NO 547: from 1 to 430

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 548
- Ceres seq\_id 1498633
- Location of start within SEQ ID NO 546: at 217 nt.



(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5808
- gi No. 4455180
- % Identity 92.8
- Alignment Length 432
- Location of Alignment in SEQ ID NO 548: from 1 to 378

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 549
- Ceres seq\_id 1498634
- Location of start within SEQ ID NO 546: at 319 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 5809
- gi No. 4455180
- % Identity 92.8
- Alignment Length 432
- Location of Alignment in SEQ ID NO 549: from 1 to 344

Maximum Length Sequence corresponding to clone ID 126073

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 550
- Ceres seq\_id 1498635

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 551
- Ceres seq\_id 1498636
- Location of start within SEQ ID NO 550: at 282 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 5810
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 551: from 46 to 203 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5811
- gi No. 100208
- % Identity 80.7
- Alignment Length 192
- Location of Alignment in SEQ ID NO 551: from 48 to 234

- Alignment No. 5812
- gi No. 1085595
- % Identity 77
- Alignment Length 204
- Location of Alignment in SEQ ID NO 551: from 48 to 246

- Alignment No. 5813
- gi No. 1177586
- % Identity 78.5
- Alignment Length 191
- Location of Alignment in SEQ ID NO 551: from 48 to 234

- Alignment No. 5814
- gi No. 119181
- % Identity 79.1
- Alignment Length 196

- Location of Alignment in SEQ ID NO 551: from 48 to 242
- Alignment No. 5815
- gi No. 119639
- % Identity 77.7
- Alignment Length 193
- Location of Alignment in SEQ ID NO 551: from 48 to 234
- Alignment No. 5816
- gi No. 129646
- % Identity 73.7
- Alignment Length 205
- Location of Alignment in SEQ ID NO 551: from 48 to 244
- Alignment No. 5817
- gi No. 1314707
- % Identity 76.1
- Alignment Length 205
- Location of Alignment in SEQ ID NO 551: from 48 to 246
- Alignment No. 5818
- gi No. 1326182
- % Identity 73.2
- Alignment Length 206
- Location of Alignment in SEQ ID NO 551: from 47 to 246
- Alignment No. 5819
- gi No. 1339998
- % Identity 88.1
- Alignment Length 59
- Location of Alignment in SEQ ID NO 551: from 101 to 159
- Alignment No. 5820
- gi No. 1369763
- % Identity 78.5
- Alignment Length 195
- Location of Alignment in SEQ ID NO 551: from 48 to 237
- Alignment No. 5821
- gi No. 1458104
- % Identity 78.4
- Alignment Length 190
- Location of Alignment in SEQ ID NO 551: from 48 to 232
- Alignment No. 5822
- gi No. 1458106
- % Identity 76.5
- Alignment Length 187
- Location of Alignment in SEQ ID NO 551: from 48 to 230
- Alignment No. 5823
- gi No. 1458108
- % Identity 79.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 551: from 48 to 106
- Alignment No. 5824
- gi No. 1469799
- % Identity 75.1
- Alignment Length 205
- Location of Alignment in SEQ ID NO 551: from 48 to 246

- Alignment No. 5825
- gi No. 1527191
- % Identity 78
- Alignment Length 191
- Location of Alignment in SEQ ID NO 551: from 48 to 234
  
- Alignment No. 5826
- gi No. 1703057
- % Identity 76.2
- Alignment Length 207
- Location of Alignment in SEQ ID NO 551: from 48 to 248
  
- Alignment No. 5827
- gi No. 1743374
- % Identity 78
- Alignment Length 203
- Location of Alignment in SEQ ID NO 551: from 48 to 246
  
- Alignment No. 5828
- gi No. 1813891
- % Identity 77.5
- Alignment Length 204
- Location of Alignment in SEQ ID NO 551: from 47 to 246
  
- Alignment No. 5829
- gi No. 1944152
- % Identity 74.2
- Alignment Length 198
- Location of Alignment in SEQ ID NO 551: from 47 to 239
  
- Alignment No. 5830
- gi No. 2274778
- % Identity 74.4
- Alignment Length 207
- Location of Alignment in SEQ ID NO 551: from 47 to 248
  
- Alignment No. 5831
- gi No. 232041
- % Identity 78
- Alignment Length 191
- Location of Alignment in SEQ ID NO 551: from 48 to 234
  
- Alignment No. 5832
- gi No. 2385371
- % Identity 78
- Alignment Length 191
- Location of Alignment in SEQ ID NO 551: from 48 to 234
  
- Alignment No. 5833
- gi No. 2414153
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 551: from 48 to 83
  
- Alignment No. 5834
- gi No. 2492612
- % Identity 71.1
- Alignment Length 197
- Location of Alignment in SEQ ID NO 551: from 48 to 240

- Alignment No. 5835
- gi No. 2735955
- % Identity 78
- Alignment Length 191
- Location of Alignment in SEQ ID NO 551: from 48 to 234
  
- Alignment No. 5836
- gi No. 2769652
- % Identity 72.7
- Alignment Length 206
- Location of Alignment in SEQ ID NO 551: from 47 to 246
  
- Alignment No. 5837
- gi No. 2781354
- % Identity 100
- Alignment Length 206
- Location of Alignment in SEQ ID NO 551: from 46 to 251
  
- Alignment No. 5838
- gi No. 2801541
- % Identity 79.1
- Alignment Length 191
- Location of Alignment in SEQ ID NO 551: from 48 to 234
  
- Alignment No. 5839
- gi No. 2826769
- % Identity 77.9
- Alignment Length 204
- Location of Alignment in SEQ ID NO 551: from 48 to 246
  
- Alignment No. 5840
- gi No. 2952326
- % Identity 73.3
- Alignment Length 191
- Location of Alignment in SEQ ID NO 551: from 48 to 234
  
- Alignment No. 5841
- gi No. 300266
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 551: from 111 to 132
  
- Alignment No. 5842
- gi No. 3025693
- % Identity 75.5
- Alignment Length 163
- Location of Alignment in SEQ ID NO 551: from 46 to 206
  
- Alignment No. 5843
- gi No. 3025697
- % Identity 72.8
- Alignment Length 231
- Location of Alignment in SEQ ID NO 551: from 25 to 246
  
- Alignment No. 5844
- gi No. 3037047
- % Identity 73.3
- Alignment Length 195
- Location of Alignment in SEQ ID NO 551: from 48 to 237
  
- Alignment No. 5845

- gi No. 3157930
- % Identity 88.8
- Alignment Length 205
- Location of Alignment in SEQ ID NO 551: from 47 to 251
  
- Alignment No. 5846
- gi No. 3341717
- % Identity 99.5
- Alignment Length 206
- Location of Alignment in SEQ ID NO 551: from 46 to 251
  
- Alignment No. 5847
- gi No. 3641651
- % Identity 72.8
- Alignment Length 231
- Location of Alignment in SEQ ID NO 551: from 25 to 246
  
- Alignment No. 5848
- gi No. 3641653
- % Identity 72.1
- Alignment Length 206
- Location of Alignment in SEQ ID NO 551: from 46 to 248
  
- Alignment No. 5849
- gi No. 3779220
- % Identity 75.7
- Alignment Length 207
- Location of Alignment in SEQ ID NO 551: from 48 to 248
  
- Alignment No. 5850
- gi No. 398992
- % Identity 80.7
- Alignment Length 192
- Location of Alignment in SEQ ID NO 551: from 48 to 234
  
- Alignment No. 5851
- gi No. 398994
- % Identity 74.4
- Alignment Length 207
- Location of Alignment in SEQ ID NO 551: from 47 to 248
  
- Alignment No. 5852
- gi No. 398995
- % Identity 74.8
- Alignment Length 203
- Location of Alignment in SEQ ID NO 551: from 48 to 246
  
- Alignment No. 5853
- gi No. 398996
- % Identity 73.8
- Alignment Length 210
- Location of Alignment in SEQ ID NO 551: from 46 to 244
  
- Alignment No. 5854
- gi No. 398997
- % Identity 75
- Alignment Length 204
- Location of Alignment in SEQ ID NO 551: from 48 to 248
  
- Alignment No. 5855
- gi No. 4056424

- % Identity 71.6
- Alignment Length 212
- Location of Alignment in SEQ ID NO 551: from 46 to 250
  
- Alignment No. 5856
- gi No. 4090533
- % Identity 78.4
- Alignment Length 199
- Location of Alignment in SEQ ID NO 551: from 47 to 240
  
- Alignment No. 5857
- gi No. 4104679
- % Identity 73.4
- Alignment Length 207
- Location of Alignment in SEQ ID NO 551: from 46 to 244
  
- Alignment No. 5858
- gi No. 4164153
- % Identity 74.6
- Alignment Length 181
- Location of Alignment in SEQ ID NO 551: from 48 to 223
  
- Alignment No. 5859
- gi No. 416569
- % Identity 72.9
- Alignment Length 232
- Location of Alignment in SEQ ID NO 551: from 25 to 246
  
- Alignment No. 5860
- gi No. 445588
- % Identity 77.5
- Alignment Length 204
- Location of Alignment in SEQ ID NO 551: from 48 to 246
  
- Alignment No. 5861
- gi No. 458338
- % Identity 78.1
- Alignment Length 196
- Location of Alignment in SEQ ID NO 551: from 48 to 239
  
- Alignment No. 5862
- gi No. 458340
- % Identity 78.9
- Alignment Length 190
- Location of Alignment in SEQ ID NO 551: from 48 to 234
  
- Alignment No. 5863
- gi No. 4586409
- % Identity 78.5
- Alignment Length 191
- Location of Alignment in SEQ ID NO 551: from 48 to 234
  
- Alignment No. 5864
- gi No. 460279
- % Identity 76.8
- Alignment Length 194
- Location of Alignment in SEQ ID NO 551: from 48 to 236
  
- Alignment No. 5865
- gi No. 4704656
- % Identity 74.6

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- Alignment Length 205
- Location of Alignment in SEQ ID NO 551: from 48 to 248
  
- Alignment No. 5866
- gi No. 4704658
- % Identity 77.2
- Alignment Length 203
- Location of Alignment in SEQ ID NO 551: from 47 to 248
  
- Alignment No. 5867
- gi No. 4704660
- % Identity 75.5
- Alignment Length 192
- Location of Alignment in SEQ ID NO 551: from 48 to 234
  
- Alignment No. 5868
- gi No. 507224
- % Identity 87.9
- Alignment Length 207
- Location of Alignment in SEQ ID NO 551: from 46 to 251
  
- Alignment No. 5869
- gi No. 520802
- % Identity 75.2
- Alignment Length 203
- Location of Alignment in SEQ ID NO 551: from 48 to 246
  
- Alignment No. 5870
- gi No. 532530
- % Identity 75.6
- Alignment Length 201
- Location of Alignment in SEQ ID NO 551: from 48 to 244
  
- Alignment No. 5871
- gi No. 5360219
- % Identity 80.1
- Alignment Length 181
- Location of Alignment in SEQ ID NO 551: from 48 to 224
  
- Alignment No. 5872
- gi No. 542052
- % Identity 77.2
- Alignment Length 202
- Location of Alignment in SEQ ID NO 551: from 48 to 244
  
- Alignment No. 5873
- gi No. 543476
- % Identity 73.8
- Alignment Length 210
- Location of Alignment in SEQ ID NO 551: from 46 to 244
  
- Alignment No. 5874
- gi No. 543751
- % Identity 71.1
- Alignment Length 212
- Location of Alignment in SEQ ID NO 551: from 46 to 250
  
- Alignment No. 5875
- gi No. 559407
- % Identity 90.3
- Alignment Length 206

- Location of Alignment in SEQ ID NO 551: from 47 to 251
- Alignment No. 5876
- gi No. 560048
- % Identity 72.8
- Alignment Length 206
- Location of Alignment in SEQ ID NO 551: from 48 to 244
- Alignment No. 5877
- gi No. 584710
- % Identity 70.7
- Alignment Length 232
- Location of Alignment in SEQ ID NO 551: from 25 to 248
- Alignment No. 5878
- gi No. 584711
- % Identity 77.6
- Alignment Length 205
- Location of Alignment in SEQ ID NO 551: from 48 to 246
- Alignment No. 5879
- gi No. 584712
- % Identity 76.7
- Alignment Length 206
- Location of Alignment in SEQ ID NO 551: from 48 to 248
- Alignment No. 5880
- gi No. 587086
- % Identity 94.2
- Alignment Length 206
- Location of Alignment in SEQ ID NO 551: from 46 to 251
- Alignment No. 5881
- gi No. 602586
- % Identity 76.4
- Alignment Length 203
- Location of Alignment in SEQ ID NO 551: from 48 to 248
- Alignment No. 5882
- gi No. 629677
- % Identity 77
- Alignment Length 204
- Location of Alignment in SEQ ID NO 551: from 48 to 246
- Alignment No. 5883
- gi No. 642062
- % Identity 81.2
- Alignment Length 191
- Location of Alignment in SEQ ID NO 551: from 47 to 234
- Alignment No. 5884
- gi No. 728780
- % Identity 93.2
- Alignment Length 206
- Location of Alignment in SEQ ID NO 551: from 46 to 251

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 552
- Ceres seq\_id 1498637
- Location of start within SEQ ID NO 550: at 333 nt.



(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 5885
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 552: from 29 to 186 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5886
- gi No. 100208
- % Identity 80.7
- Alignment Length 192
- Location of Alignment in SEQ ID NO 552: from 31 to 217
- Alignment No. 5887
- gi No. 1085595
- % Identity 77
- Alignment Length 204
- Location of Alignment in SEQ ID NO 552: from 31 to 229
- Alignment No. 5888
- gi No. 1177586
- % Identity 78.5
- Alignment Length 191
- Location of Alignment in SEQ ID NO 552: from 31 to 217
- Alignment No. 5889
- gi No. 119181
- % Identity 79.1
- Alignment Length 196
- Location of Alignment in SEQ ID NO 552: from 31 to 225
- Alignment No. 5890
- gi No. 119639
- % Identity 77.7
- Alignment Length 193
- Location of Alignment in SEQ ID NO 552: from 31 to 217
- Alignment No. 5891
- gi No. 129646
- % Identity 73.7
- Alignment Length 205
- Location of Alignment in SEQ ID NO 552: from 31 to 227
- Alignment No. 5892
- gi No. 1314707
- % Identity 76.1
- Alignment Length 205
- Location of Alignment in SEQ ID NO 552: from 31 to 229
- Alignment No. 5893
- gi No. 1326182
- % Identity 73.2
- Alignment Length 206
- Location of Alignment in SEQ ID NO 552: from 30 to 229
- Alignment No. 5894
- gi No. 1339998
- % Identity 88.1
- Alignment Length 59
- Location of Alignment in SEQ ID NO 552: from 84 to 142

- Alignment No. 5895
- gi No. 1369763
- % Identity 78.5
- Alignment Length 195
- Location of Alignment in SEQ ID NO 552: from 31 to 220
  
- Alignment No. 5896
- gi No. 1458104
- % Identity 78.4
- Alignment Length 190
- Location of Alignment in SEQ ID NO 552: from 31 to 215
  
- Alignment No. 5897
- gi No. 1458106
- % Identity 76.5
- Alignment Length 187
- Location of Alignment in SEQ ID NO 552: from 31 to 213
  
- Alignment No. 5898
- gi No. 1458108
- % Identity 79.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 552: from 31 to 89
  
- Alignment No. 5899
- gi No. 1469799
- % Identity 75.1
- Alignment Length 205
- Location of Alignment in SEQ ID NO 552: from 31 to 229
  
- Alignment No. 5900
- gi No. 1527191
- % Identity 78
- Alignment Length 191
- Location of Alignment in SEQ ID NO 552: from 31 to 217
  
- Alignment No. 5901
- gi No. 1703057
- % Identity 76.2
- Alignment Length 207
- Location of Alignment in SEQ ID NO 552: from 31 to 231
  
- Alignment No. 5902
- gi No. 1743374
- % Identity 78
- Alignment Length 203
- Location of Alignment in SEQ ID NO 552: from 31 to 229
  
- Alignment No. 5903
- gi No. 1813891
- % Identity 77.5
- Alignment Length 204
- Location of Alignment in SEQ ID NO 552: from 30 to 229
  
- Alignment No. 5904
- gi No. 1944152
- % Identity 74.2
- Alignment Length 198
- Location of Alignment in SEQ ID NO 552: from 30 to 222
  
- Alignment No. 5905

- gi No. 2274778
- % Identity 74.4
- Alignment Length 207
- Location of Alignment in SEQ ID NO 552: from 30 to 231
  
- Alignment No. 5906
- gi No. 232041
- % Identity 78
- Alignment Length 191
- Location of Alignment in SEQ ID NO 552: from 31 to 217
  
- Alignment No. 5907
- gi No. 2385371
- % Identity 78
- Alignment Length 191
- Location of Alignment in SEQ ID NO 552: from 31 to 217
  
- Alignment No. 5908
- gi No. 2414153
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 552: from 31 to 66
  
- Alignment No. 5909
- gi No. 2492612
- % Identity 71.1
- Alignment Length 197
- Location of Alignment in SEQ ID NO 552: from 31 to 223
  
- Alignment No. 5910
- gi No. 2735955
- % Identity 78
- Alignment Length 191
- Location of Alignment in SEQ ID NO 552: from 31 to 217
  
- Alignment No. 5911
- gi No. 2769652
- % Identity 72.7
- Alignment Length 206
- Location of Alignment in SEQ ID NO 552: from 30 to 229
  
- Alignment No. 5912
- gi No. 2781354
- % Identity 100
- Alignment Length 206
- Location of Alignment in SEQ ID NO 552: from 29 to 234
  
- Alignment No. 5913
- gi No. 2801541
- % Identity 79.1
- Alignment Length 191
- Location of Alignment in SEQ ID NO 552: from 31 to 217
  
- Alignment No. 5914
- gi No. 2826769
- % Identity 77.9
- Alignment Length 204
- Location of Alignment in SEQ ID NO 552: from 31 to 229
  
- Alignment No. 5915
- gi No. 2952326

- % Identity 73.3
- Alignment Length 191
- Location of Alignment in SEQ ID NO 552: from 31 to 217
  
- Alignment No. 5916
- gi No. 300266
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 552: from 94 to 115
  
- Alignment No. 5917
- gi No. 3025693
- % Identity 75.5
- Alignment Length 163
- Location of Alignment in SEQ ID NO 552: from 29 to 189
  
- Alignment No. 5918
- gi No. 3025697
- % Identity 72.8
- Alignment Length 231
- Location of Alignment in SEQ ID NO 552: from 8 to 229
  
- Alignment No. 5919
- gi No. 3037047
- % Identity 73.3
- Alignment Length 195
- Location of Alignment in SEQ ID NO 552: from 31 to 220
  
- Alignment No. 5920
- gi No. 3157930
- % Identity 88.8
- Alignment Length 205
- Location of Alignment in SEQ ID NO 552: from 30 to 234
  
- Alignment No. 5921
- gi No. 3341717
- % Identity 99.5
- Alignment Length 206
- Location of Alignment in SEQ ID NO 552: from 29 to 234
  
- Alignment No. 5922
- gi No. 3641651
- % Identity 72.8
- Alignment Length 231
- Location of Alignment in SEQ ID NO 552: from 8 to 229
  
- Alignment No. 5923
- gi No. 3641653
- % Identity 72.1
- Alignment Length 206
- Location of Alignment in SEQ ID NO 552: from 29 to 231
  
- Alignment No. 5924
- gi No. 3779220
- % Identity 75.7
- Alignment Length 207
- Location of Alignment in SEQ ID NO 552: from 31 to 231
  
- Alignment No. 5925
- gi No. 398992
- % Identity 80.7

- Alignment Length 192
- Location of Alignment in SEQ ID NO 552: from 31 to 217
  
- Alignment No. 5926
- gi No. 398994
- % Identity 74.4
- Alignment Length 207
- Location of Alignment in SEQ ID NO 552: from 30 to 231
  
- Alignment No. 5927
- gi No. 398995
- % Identity 74.8
- Alignment Length 203
- Location of Alignment in SEQ ID NO 552: from 31 to 229
  
- Alignment No. 5928
- gi No. 398996
- % Identity 73.8
- Alignment Length 210
- Location of Alignment in SEQ ID NO 552: from 29 to 227
  
- Alignment No. 5929
- gi No. 398997
- % Identity 75
- Alignment Length 204
- Location of Alignment in SEQ ID NO 552: from 31 to 231
  
- Alignment No. 5930
- gi No. 4056424
- % Identity 71.6
- Alignment Length 212
- Location of Alignment in SEQ ID NO 552: from 29 to 233
  
- Alignment No. 5931
- gi No. 4090533
- % Identity 78.4
- Alignment Length 199
- Location of Alignment in SEQ ID NO 552: from 30 to 223
  
- Alignment No. 5932
- gi No. 4104679
- % Identity 73.4
- Alignment Length 207
- Location of Alignment in SEQ ID NO 552: from 29 to 227
  
- Alignment No. 5933
- gi No. 4164153
- % Identity 74.6
- Alignment Length 181
- Location of Alignment in SEQ ID NO 552: from 31 to 206
  
- Alignment No. 5934
- gi No. 416569
- % Identity 72.9
- Alignment Length 232
- Location of Alignment in SEQ ID NO 552: from 8 to 229
  
- Alignment No. 5935
- gi No. 445588
- % Identity 77.5
- Alignment Length 204

- Location of Alignment in SEQ ID NO 552: from 31 to 229
- Alignment No. 5936
- gi No. 458338
- % Identity 78.1
- Alignment Length 196
- Location of Alignment in SEQ ID NO 552: from 31 to 222
- Alignment No. 5937
- gi No. 458340
- % Identity 78.9
- Alignment Length 190
- Location of Alignment in SEQ ID NO 552: from 31 to 217
- Alignment No. 5938
- gi No. 4586409
- % Identity 78.5
- Alignment Length 191
- Location of Alignment in SEQ ID NO 552: from 31 to 217
- Alignment No. 5939
- gi No. 460279
- % Identity 76.8
- Alignment Length 194
- Location of Alignment in SEQ ID NO 552: from 31 to 219
- Alignment No. 5940
- gi No. 4704656
- % Identity 74.6
- Alignment Length 205
- Location of Alignment in SEQ ID NO 552: from 31 to 231
- Alignment No. 5941
- gi No. 4704658
- % Identity 77.2
- Alignment Length 203
- Location of Alignment in SEQ ID NO 552: from 30 to 231
- Alignment No. 5942
- gi No. 4704660
- % Identity 75.5
- Alignment Length 192
- Location of Alignment in SEQ ID NO 552: from 31 to 217
- Alignment No. 5943
- gi No. 507224
- % Identity 87.9
- Alignment Length 207
- Location of Alignment in SEQ ID NO 552: from 29 to 234
- Alignment No. 5944
- gi No. 520802
- % Identity 75.2
- Alignment Length 203
- Location of Alignment in SEQ ID NO 552: from 31 to 229
- Alignment No. 5945
- gi No. 532530
- % Identity 75.6
- Alignment Length 201
- Location of Alignment in SEQ ID NO 552: from 31 to 227

- Alignment No. 5946
- gi No. 5360219
- % Identity 80.1
- Alignment Length 181
- Location of Alignment in SEQ ID NO 552: from 31 to 207
  
- Alignment No. 5947
- gi No. 542052
- % Identity 77.2
- Alignment Length 202
- Location of Alignment in SEQ ID NO 552: from 31 to 227
  
- Alignment No. 5948
- gi No. 543476
- % Identity 73.8
- Alignment Length 210
- Location of Alignment in SEQ ID NO 552: from 29 to 227
  
- Alignment No. 5949
- gi No. 543751
- % Identity 71.1
- Alignment Length 212
- Location of Alignment in SEQ ID NO 552: from 29 to 233
  
- Alignment No. 5950
- gi No. 559407
- % Identity 90.3
- Alignment Length 206
- Location of Alignment in SEQ ID NO 552: from 30 to 234
  
- Alignment No. 5951
- gi No. 560048
- % Identity 72.8
- Alignment Length 206
- Location of Alignment in SEQ ID NO 552: from 31 to 227
  
- Alignment No. 5952
- gi No. 584710
- % Identity 70.7
- Alignment Length 232
- Location of Alignment in SEQ ID NO 552: from 8 to 231
  
- Alignment No. 5953
- gi No. 584711
- % Identity 77.6
- Alignment Length 205
- Location of Alignment in SEQ ID NO 552: from 31 to 229
  
- Alignment No. 5954
- gi No. 584712
- % Identity 76.7
- Alignment Length 206
- Location of Alignment in SEQ ID NO 552: from 31 to 231
  
- Alignment No. 5955
- gi No. 587086
- % Identity 94.2
- Alignment Length 206
- Location of Alignment in SEQ ID NO 552: from 29 to 234

- Alignment No. 5956
- gi No. 602586
- % Identity 76.4
- Alignment Length 203
- Location of Alignment in SEQ ID NO 552: from 31 to 231
  
- Alignment No. 5957
- gi No. 629677
- % Identity 77
- Alignment Length 204
- Location of Alignment in SEQ ID NO 552: from 31 to 229
  
- Alignment No. 5958
- gi No. 642062
- % Identity 81.2
- Alignment Length 191
- Location of Alignment in SEQ ID NO 552: from 30 to 217
  
- Alignment No. 5959
- gi No. 728780
- % Identity 93.2
- Alignment Length 206
- Location of Alignment in SEQ ID NO 552: from 29 to 234

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 553
- Ceres seq\_id 1498638
- Location of start within SEQ ID NO 550: at 387 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 5960
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 553: from 11 to 168 aa.

(D) Related Amino Acid Sequences

- Alignment No. 5961
- gi No. 100208
- % Identity 80.7
- Alignment Length 192
- Location of Alignment in SEQ ID NO 553: from 13 to 199
  
- Alignment No. 5962
- gi No. 1085595
- % Identity 77
- Alignment Length 204
- Location of Alignment in SEQ ID NO 553: from 13 to 211
  
- Alignment No. 5963
- gi No. 1177586
- % Identity 78.5
- Alignment Length 191
- Location of Alignment in SEQ ID NO 553: from 13 to 199
  
- Alignment No. 5964
- gi No. 119181
- % Identity 79.1
- Alignment Length 196
- Location of Alignment in SEQ ID NO 553: from 13 to 207
  
- Alignment No. 5965



- gi No. 119639
- % Identity 77.7
- Alignment Length 193
- Location of Alignment in SEQ ID NO 553: from 13 to 199
  
- Alignment No. 5966
- gi No. 129646
- % Identity 73.7
- Alignment Length 205
- Location of Alignment in SEQ ID NO 553: from 13 to 209
  
- Alignment No. 5967
- gi No. 1314707
- % Identity 76.1
- Alignment Length 205
- Location of Alignment in SEQ ID NO 553: from 13 to 211
  
- Alignment No. 5968
- gi No. 1326182
- % Identity 73.2
- Alignment Length 206
- Location of Alignment in SEQ ID NO 553: from 12 to 211
  
- Alignment No. 5969
- gi No. 1339998
- % Identity 88.1
- Alignment Length 59
- Location of Alignment in SEQ ID NO 553: from 66 to 124
  
- Alignment No. 5970
- gi No. 1369763
- % Identity 78.5
- Alignment Length 195
- Location of Alignment in SEQ ID NO 553: from 13 to 202
  
- Alignment No. 5971
- gi No. 1458104
- % Identity 78.4
- Alignment Length 190
- Location of Alignment in SEQ ID NO 553: from 13 to 197
  
- Alignment No. 5972
- gi No. 1458106
- % Identity 76.5
- Alignment Length 187
- Location of Alignment in SEQ ID NO 553: from 13 to 195
  
- Alignment No. 5973
- gi No. 1458108
- % Identity 79.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 553: from 13 to 71
  
- Alignment No. 5974
- gi No. 1469799
- % Identity 75.1
- Alignment Length 205
- Location of Alignment in SEQ ID NO 553: from 13 to 211
  
- Alignment No. 5975
- gi No. 1527191

- % Identity 78
- Alignment Length 191
- Location of Alignment in SEQ ID NO 553: from 13 to 199
  
- Alignment No. 5976
- gi No. 1703057
- % Identity 76.2
- Alignment Length 207
- Location of Alignment in SEQ ID NO 553: from 13 to 213
  
- Alignment No. 5977
- gi No. 1743374
- % Identity 78
- Alignment Length 203
- Location of Alignment in SEQ ID NO 553: from 13 to 211
  
- Alignment No. 5978
- gi No. 1813891
- % Identity 77.5
- Alignment Length 204
- Location of Alignment in SEQ ID NO 553: from 12 to 211
  
- Alignment No. 5979
- gi No. 1944152
- % Identity 74.2
- Alignment Length 198
- Location of Alignment in SEQ ID NO 553: from 12 to 204
  
- Alignment No. 5980
- gi No. 2274778
- % Identity 74.4
- Alignment Length 207
- Location of Alignment in SEQ ID NO 553: from 12 to 213
  
- Alignment No. 5981
- gi No. 232041
- % Identity 78
- Alignment Length 191
- Location of Alignment in SEQ ID NO 553: from 13 to 199
  
- Alignment No. 5982
- gi No. 2385371
- % Identity 78
- Alignment Length 191
- Location of Alignment in SEQ ID NO 553: from 13 to 199
  
- Alignment No. 5983
- gi No. 2414153
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 553: from 13 to 48
  
- Alignment No. 5984
- gi No. 2492612
- % Identity 71.1
- Alignment Length 197
- Location of Alignment in SEQ ID NO 553: from 13 to 205
  
- Alignment No. 5985
- gi No. 2735955
- % Identity 78

- Alignment Length 191
- Location of Alignment in SEQ ID NO 553: from 13 to 199
  
- Alignment No. 5986
- gi No. 2769652
- % Identity 72.7
- Alignment Length 206
- Location of Alignment in SEQ ID NO 553: from 12 to 211
  
- Alignment No. 5987
- gi No. 2781354
- % Identity 100
- Alignment Length 206
- Location of Alignment in SEQ ID NO 553: from 11 to 216
  
- Alignment No. 5988
- gi No. 2801541
- % Identity 79.1
- Alignment Length 191
- Location of Alignment in SEQ ID NO 553: from 13 to 199
  
- Alignment No. 5989
- gi No. 2826769
- % Identity 77.9
- Alignment Length 204
- Location of Alignment in SEQ ID NO 553: from 13 to 211
  
- Alignment No. 5990
- gi No. 2952326
- % Identity 73.3
- Alignment Length 191
- Location of Alignment in SEQ ID NO 553: from 13 to 199
  
- Alignment No. 5991
- gi No. 300266
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 553: from 76 to 97
  
- Alignment No. 5992
- gi No. 3025693
- % Identity 75.5
- Alignment Length 163
- Location of Alignment in SEQ ID NO 553: from 11 to 171
  
- Alignment No. 5993
- gi No. 3025697
- % Identity 72.8
- Alignment Length 231
- Location of Alignment in SEQ ID NO 553: from 1 to 211
  
- Alignment No. 5994
- gi No. 3037047
- % Identity 73.3
- Alignment Length 195
- Location of Alignment in SEQ ID NO 553: from 13 to 202
  
- Alignment No. 5995
- gi No. 3157930
- % Identity 88.8
- Alignment Length 205

- Location of Alignment in SEQ ID NO 553: from 12 to 216
- Alignment No. 5996
- gi No. 3341717
- % Identity 99.5
- Alignment Length 206
- Location of Alignment in SEQ ID NO 553: from 11 to 216
- Alignment No. 5997
- gi No. 3641651
- % Identity 72.8
- Alignment Length 231
- Location of Alignment in SEQ ID NO 553: from 1 to 211
- Alignment No. 5998
- gi No. 3641653
- % Identity 72.1
- Alignment Length 206
- Location of Alignment in SEQ ID NO 553: from 11 to 213
- Alignment No. 5999
- gi No. 3779220
- % Identity 75.7
- Alignment Length 207
- Location of Alignment in SEQ ID NO 553: from 13 to 213
- Alignment No. 6000
- gi No. 398992
- % Identity 80.7
- Alignment Length 192
- Location of Alignment in SEQ ID NO 553: from 13 to 199
- Alignment No. 6001
- gi No. 398994
- % Identity 74.4
- Alignment Length 207
- Location of Alignment in SEQ ID NO 553: from 12 to 213
- Alignment No. 6002
- gi No. 398995
- % Identity 74.8
- Alignment Length 203
- Location of Alignment in SEQ ID NO 553: from 13 to 211
- Alignment No. 6003
- gi No. 398996
- % Identity 73.8
- Alignment Length 210
- Location of Alignment in SEQ ID NO 553: from 11 to 209
- Alignment No. 6004
- gi No. 398997
- % Identity 75
- Alignment Length 204
- Location of Alignment in SEQ ID NO 553: from 13 to 213
- Alignment No. 6005
- gi No. 4056424
- % Identity 71.6
- Alignment Length 212
- Location of Alignment in SEQ ID NO 553: from 11 to 215

- Alignment No. 6006
- gi No. 4090533
- % Identity 78.4
- Alignment Length 199
- Location of Alignment in SEQ ID NO 553: from 12 to 205
  
- Alignment No. 6007
- gi No. 4104679
- % Identity 73.4
- Alignment Length 207
- Location of Alignment in SEQ ID NO 553: from 11 to 209
  
- Alignment No. 6008
- gi No. 4164153
- % Identity 74.6
- Alignment Length 181
- Location of Alignment in SEQ ID NO 553: from 13 to 188
  
- Alignment No. 6009
- gi No. 416569
- % Identity 72.9
- Alignment Length 232
- Location of Alignment in SEQ ID NO 553: from 1 to 211
  
- Alignment No. 6010
- gi No. 445588
- % Identity 77.5
- Alignment Length 204
- Location of Alignment in SEQ ID NO 553: from 13 to 211
  
- Alignment No. 6011
- gi No. 458338
- % Identity 78.1
- Alignment Length 196
- Location of Alignment in SEQ ID NO 553: from 13 to 204
  
- Alignment No. 6012
- gi No. 458340
- % Identity 78.9
- Alignment Length 190
- Location of Alignment in SEQ ID NO 553: from 13 to 199
  
- Alignment No. 6013
- gi No. 4586409
- % Identity 78.5
- Alignment Length 191
- Location of Alignment in SEQ ID NO 553: from 13 to 199
  
- Alignment No. 6014
- gi No. 460279
- % Identity 76.8
- Alignment Length 194
- Location of Alignment in SEQ ID NO 553: from 13 to 201
  
- Alignment No. 6015
- gi No. 4704656
- % Identity 74.6
- Alignment Length 205
- Location of Alignment in SEQ ID NO 553: from 13 to 213

- Alignment No. 6016
- gi No. 4704658
- % Identity 77.2
- Alignment Length 203
- Location of Alignment in SEQ ID NO 553: from 12 to 213
  
- Alignment No. 6017
- gi No. 4704660
- % Identity 75.5
- Alignment Length 192
- Location of Alignment in SEQ ID NO 553: from 13 to 199
  
- Alignment No. 6018
- gi No. 507224
- % Identity 87.9
- Alignment Length 207
- Location of Alignment in SEQ ID NO 553: from 11 to 216
  
- Alignment No. 6019
- gi No. 520802
- % Identity 75.2
- Alignment Length 203
- Location of Alignment in SEQ ID NO 553: from 13 to 211
  
- Alignment No. 6020
- gi No. 532530
- % Identity 75.6
- Alignment Length 201
- Location of Alignment in SEQ ID NO 553: from 13 to 209
  
- Alignment No. 6021
- gi No. 5360219
- % Identity 80.1
- Alignment Length 181
- Location of Alignment in SEQ ID NO 553: from 13 to 189
  
- Alignment No. 6022
- gi No. 542052
- % Identity 77.2
- Alignment Length 202
- Location of Alignment in SEQ ID NO 553: from 13 to 209
  
- Alignment No. 6023
- gi No. 543476
- % Identity 73.8
- Alignment Length 210
- Location of Alignment in SEQ ID NO 553: from 11 to 209
  
- Alignment No. 6024
- gi No. 543751
- % Identity 71.1
- Alignment Length 212
- Location of Alignment in SEQ ID NO 553: from 11 to 215
  
- Alignment No. 6025
- gi No. 559407
- % Identity 90.3
- Alignment Length 206
- Location of Alignment in SEQ ID NO 553: from 12 to 216
  
- Alignment No. 6026

- gi No. 560048
- % Identity 72.8
- Alignment Length 206
- Location of Alignment in SEQ ID NO 553: from 13 to 209
  
- Alignment No. 6027
- gi No. 584710
- % Identity 70.7
- Alignment Length 232
- Location of Alignment in SEQ ID NO 553: from 1 to 213
  
- Alignment No. 6028
- gi No. 584711
- % Identity 77.6
- Alignment Length 205
- Location of Alignment in SEQ ID NO 553: from 13 to 211
  
- Alignment No. 6029
- gi No. 584712
- % Identity 76.7
- Alignment Length 206
- Location of Alignment in SEQ ID NO 553: from 13 to 213
  
- Alignment No. 6030
- gi No. 587086
- % Identity 94.2
- Alignment Length 206
- Location of Alignment in SEQ ID NO 553: from 11 to 216
  
- Alignment No. 6031
- gi No. 602586
- % Identity 76.4
- Alignment Length 203
- Location of Alignment in SEQ ID NO 553: from 13 to 213
  
- Alignment No. 6032
- gi No. 629677
- % Identity 77
- Alignment Length 204
- Location of Alignment in SEQ ID NO 553: from 13 to 211
  
- Alignment No. 6033
- gi No. 642062
- % Identity 81.2
- Alignment Length 191
- Location of Alignment in SEQ ID NO 553: from 12 to 199
  
- Alignment No. 6034
- gi No. 728780
- % Identity 93.2
- Alignment Length 206
- Location of Alignment in SEQ ID NO 553: from 11 to 216

Maximum Length Sequence corresponding to clone ID 126278

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 554
- Ceres seq\_id 1498639

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 555
- Ceres seq\_id 1498640
- Location of start within SEQ ID NO 554: at 46 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6035
- ER lumen protein retaining receptor
- Location within SEQ ID NO 555: from 44 to 255 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6036
- gi No. 4490331
- % Identity 87.8
- Alignment Length 139
- Location of Alignment in SEQ ID NO 555: from 2 to 140

- Alignment No. 6037
- gi No. 4803924
- % Identity 94.5
- Alignment Length 256
- Location of Alignment in SEQ ID NO 555: from 1 to 256

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 556
- Ceres seq\_id 1498641
- Location of start within SEQ ID NO 554: at 130 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6038
- ER lumen protein retaining receptor
- Location within SEQ ID NO 556: from 16 to 227 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6039
- gi No. 4490331
- % Identity 87.8
- Alignment Length 139
- Location of Alignment in SEQ ID NO 556: from 1 to 112

- Alignment No. 6040
- gi No. 4803924
- % Identity 94.5
- Alignment Length 256
- Location of Alignment in SEQ ID NO 556: from 1 to 228

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 557
- Ceres seq\_id 1498642
- Location of start within SEQ ID NO 554: at 238 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6041
- ER lumen protein retaining receptor
- Location within SEQ ID NO 557: from 1 to 191 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6042
- gi No. 4490331
- % Identity 87.8
- Alignment Length 139
- Location of Alignment in SEQ ID NO 557: from 1 to 76

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- Alignment No. 6043
- gi No. 4803924
- % Identity 94.5
- Alignment Length 256
- Location of Alignment in SEQ ID NO 557: from 1 to 192

Maximum Length Sequence corresponding to clone ID 126568

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 558
- Ceres seq\_id 1498643

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 559
- Ceres seq\_id 1498644
- Location of start within SEQ ID NO 558: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6044
- gi No. 3738296
- % Identity 100
- Alignment Length 208
- Location of Alignment in SEQ ID NO 559: from 11 to 218

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 560
- Ceres seq\_id 1498645
- Location of start within SEQ ID NO 558: at 31 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6045
- gi No. 3738296
- % Identity 100
- Alignment Length 208
- Location of Alignment in SEQ ID NO 560: from 1 to 208

Maximum Length Sequence corresponding to clone ID 126655

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 561
- Ceres seq\_id 1498646

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 562
- Ceres seq\_id 1498647
- Location of start within SEQ ID NO 561: at 99 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6046
- UDP-glucuronosyl and UDP-glucosyl transferases
- Location within SEQ ID NO 562: from 237 to 393 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6047
- gi No. 2191136
- % Identity 100
- Alignment Length 145
- Location of Alignment in SEQ ID NO 562: from 1 to 145

- Alignment No. 6048
- gi No. 2191136
- % Identity 93.3
- Alignment Length 344
- Location of Alignment in SEQ ID NO 562: from 138 to 480

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 563
- Ceres seq\_id 1498648
- Location of start within SEQ ID NO 561: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6049
- UDP-glucuronosyl and UDP-glucosyl transferases
- Location within SEQ ID NO 563: from 221 to 377 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6050
- gi No. 2191136
- % Identity 100
- Alignment Length 145
- Location of Alignment in SEQ ID NO 563: from 1 to 129
- Alignment No. 6051
- gi No. 2191136
- % Identity 93.3
- Alignment Length 344
- Location of Alignment in SEQ ID NO 563: from 122 to 464

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 564
- Ceres seq\_id 1498649
- Location of start within SEQ ID NO 561: at 606 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6052
- UDP-glucuronosyl and UDP-glucosyl transferases
- Location within SEQ ID NO 564: from 68 to 224 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6053
- gi No. 2191136
- % Identity 93.3
- Alignment Length 344
- Location of Alignment in SEQ ID NO 564: from 1 to 311

Maximum Length Sequence corresponding to clone ID 141805

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 565
- Ceres seq\_id 1498650

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 566
- Ceres seq\_id 1498651
- Location of start within SEQ ID NO 565: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6054
- Dehydrogenase E1 component

- Location within SEQ ID NO 566: from 123 to 427 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6055
- gi No. 2454182
- % Identity 100
- Alignment Length 428
- Location of Alignment in SEQ ID NO 566: from 35 to 462

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 567
- Ceres seq\_id 1498652
- Location of start within SEQ ID NO 565: at 105 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6056
- Dehydrogenase E1 component
- Location within SEQ ID NO 567: from 89 to 393 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6057
- gi No. 2454182
- % Identity 100
- Alignment Length 428
- Location of Alignment in SEQ ID NO 567: from 1 to 428

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 568
- Ceres seq\_id 1498653
- Location of start within SEQ ID NO 565: at 375 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6058
- Dehydrogenase E1 component
- Location within SEQ ID NO 568: from 1 to 303 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6059
- gi No. 2454182
- % Identity 100
- Alignment Length 428
- Location of Alignment in SEQ ID NO 568: from 1 to 338

Maximum Length Sequence corresponding to clone ID 142045

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 569
- Ceres seq\_id 1498654

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 570
- Ceres seq\_id 1498655
- Location of start within SEQ ID NO 569: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6060
- gi No. 4678940
- % Identity 99.2
- Alignment Length 362

- Location of Alignment in SEQ ID NO 570: from 13 to 374

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 571
- Ceres seq\_id 1498656
- Location of start within SEQ ID NO 569: at 37 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6061
- gi No. 4678940
- % Identity 99.2
- Alignment Length 362
- Location of Alignment in SEQ ID NO 571: from 1 to 362

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 572
- Ceres seq\_id 1498657
- Location of start within SEQ ID NO 569: at 430 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6062
- gi No. 4678940
- % Identity 99.2
- Alignment Length 362
- Location of Alignment in SEQ ID NO 572: from 1 to 231

Maximum Length Sequence corresponding to clone ID 142634

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 573
- Ceres seq\_id 1498658

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 574
- Ceres seq\_id 1498659
- Location of start within SEQ ID NO 573: at 25 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6063
- Glycosyl hydrolases family 16
- Location within SEQ ID NO 574: from 27 to 216 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6064
- gi No. 2244732
- % Identity 77.1
- Alignment Length 275
- Location of Alignment in SEQ ID NO 574: from 15 to 289
- Alignment No. 6065
- gi No. 2827712
- % Identity 79.2
- Alignment Length 265
- Location of Alignment in SEQ ID NO 574: from 27 to 291
- Alignment No. 6066
- gi No. 4490725
- % Identity 99.7

- Alignment Length 293
- Location of Alignment in SEQ ID NO 574: from 1 to 293
- Alignment No. 6067
- gi No. 5070246
- % Identity 76
- Alignment Length 267
- Location of Alignment in SEQ ID NO 574: from 27 to 293

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 575
- Ceres seq\_id 1498660
- Location of start within SEQ ID NO 573: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6068
- Glycosyl hydrolases family 16
- Location within SEQ ID NO 575: from 1 to 189 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6069
- gi No. 2244732
- % Identity 77.1
- Alignment Length 275
- Location of Alignment in SEQ ID NO 575: from 1 to 262
- Alignment No. 6070
- gi No. 2827712
- % Identity 79.2
- Alignment Length 265
- Location of Alignment in SEQ ID NO 575: from 1 to 264
- Alignment No. 6071
- gi No. 4490725
- % Identity 99.7
- Alignment Length 293
- Location of Alignment in SEQ ID NO 575: from 1 to 266
- Alignment No. 6072
- gi No. 5070246
- % Identity 76
- Alignment Length 267
- Location of Alignment in SEQ ID NO 575: from 1 to 266

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 576
- Ceres seq\_id 1498661
- Location of start within SEQ ID NO 573: at 265 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6073
- Glycosyl hydrolases family 16
- Location within SEQ ID NO 576: from 1 to 136 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6074
- gi No. 2244732
- % Identity 77.1
- Alignment Length 275

- Location of Alignment in SEQ ID NO 576: from 1 to 209
- Alignment No. 6075
- gi No. 2827712
- % Identity 79.2
- Alignment Length 265
- Location of Alignment in SEQ ID NO 576: from 1 to 211
- Alignment No. 6076
- gi No. 4490725
- % Identity 99.7
- Alignment Length 293
- Location of Alignment in SEQ ID NO 576: from 1 to 213
- Alignment No. 6077
- gi No. 5070246
- % Identity 76
- Alignment Length 267
- Location of Alignment in SEQ ID NO 576: from 1 to 213

Maximum Length Sequence corresponding to clone ID 142681

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 577
- Ceres seq\_id 1498662

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 578
- Ceres seq\_id 1498663
- Location of start within SEQ ID NO 577: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6078
- gi No. 100361
- % Identity 71.4
- Alignment Length 237
- Location of Alignment in SEQ ID NO 578: from 1 to 231
- Alignment No. 6079
- gi No. 100362
- % Identity 78.8
- Alignment Length 231
- Location of Alignment in SEQ ID NO 578: from 6 to 231
- Alignment No. 6080
- gi No. 100363
- % Identity 78.3
- Alignment Length 166
- Location of Alignment in SEQ ID NO 578: from 1 to 161
- Alignment No. 6081
- gi No. 131390
- % Identity 72.3
- Alignment Length 231
- Location of Alignment in SEQ ID NO 578: from 1 to 231
- Alignment No. 6082
- gi No. 131391
- % Identity 88.7
- Alignment Length 231
- Location of Alignment in SEQ ID NO 578: from 1 to 231

- Alignment No. 6083
- gi No. 131392
- % Identity 71.9
- Alignment Length 236
- Location of Alignment in SEQ ID NO 578: from 1 to 231
  
- Alignment No. 6084
- gi No. 131393
- % Identity 74.2
- Alignment Length 237
- Location of Alignment in SEQ ID NO 578: from 1 to 231
  
- Alignment No. 6085
- gi No. 1620920
- % Identity 90.8
- Alignment Length 185
- Location of Alignment in SEQ ID NO 578: from 47 to 231
  
- Alignment No. 6086
- gi No. 1769905
- % Identity 99.1
- Alignment Length 231
- Location of Alignment in SEQ ID NO 578: from 1 to 231
  
- Alignment No. 6087
- gi No. 1771778
- % Identity 77.4
- Alignment Length 233
- Location of Alignment in SEQ ID NO 578: from 2 to 231
  
- Alignment No. 6088
- gi No. 266856
- % Identity 77.8
- Alignment Length 231
- Location of Alignment in SEQ ID NO 578: from 2 to 231
  
- Alignment No. 6089
- gi No. 280370
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 578: from 78 to 98
  
- Alignment No. 6090
- gi No. 2880056
- % Identity 80.5
- Alignment Length 232
- Location of Alignment in SEQ ID NO 578: from 1 to 231
  
- Alignment No. 6091
- gi No. 2921508
- % Identity 70.3
- Alignment Length 234
- Location of Alignment in SEQ ID NO 578: from 1 to 231
  
- Alignment No. 6092
- gi No. 625545
- % Identity 81.5
- Alignment Length 173
- Location of Alignment in SEQ ID NO 578: from 59 to 231

- Alignment No. 6093
- gi No. 625546
- % Identity 77.5
- Alignment Length 238
- Location of Alignment in SEQ ID NO 578: from 1 to 231
  
- Alignment No. 6094
- gi No. 81477
- % Identity 88.2
- Alignment Length 17
- Location of Alignment in SEQ ID NO 578: from 79 to 95
  
- Alignment No. 6095
- gi No. 81723
- % Identity 88.1
- Alignment Length 219
- Location of Alignment in SEQ ID NO 578: from 13 to 231
  
- Alignment No. 6096
- gi No. 81935
- % Identity 86.1
- Alignment Length 36
- Location of Alignment in SEQ ID NO 578: from 78 to 113
  
- Alignment No. 6097
- gi No. 82188
- % Identity 79
- Alignment Length 229
- Location of Alignment in SEQ ID NO 578: from 1 to 224
  
- Alignment No. 6098
- gi No. 82189
- % Identity 79
- Alignment Length 229
- Location of Alignment in SEQ ID NO 578: from 8 to 231
  
- Alignment No. 6099
- gi No. 82498
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 578: from 78 to 113

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 579
- Ceres seq\_id 1498664
- Location of start within SEQ ID NO 577: at 476 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6100
- gi No. 100361
- % Identity 71.4
- Alignment Length 237
- Location of Alignment in SEQ ID NO 579: from 1 to 93
  
- Alignment No. 6101
- gi No. 100362
- % Identity 78.8
- Alignment Length 231
- Location of Alignment in SEQ ID NO 579: from 1 to 93



- Alignment No. 6102
- gi No. 100363
- % Identity 78.3
- Alignment Length 166
- Location of Alignment in SEQ ID NO 579: from 1 to 23
  
- Alignment No. 6103
- gi No. 131390
- % Identity 72.3
- Alignment Length 231
- Location of Alignment in SEQ ID NO 579: from 1 to 93
  
- Alignment No. 6104
- gi No. 131391
- % Identity 88.7
- Alignment Length 231
- Location of Alignment in SEQ ID NO 579: from 1 to 93
  
- Alignment No. 6105
- gi No. 131392
- % Identity 71.9
- Alignment Length 236
- Location of Alignment in SEQ ID NO 579: from 1 to 93
  
- Alignment No. 6106
- gi No. 131393
- % Identity 74.2
- Alignment Length 237
- Location of Alignment in SEQ ID NO 579: from 1 to 93
  
- Alignment No. 6107
- gi No. 1620920
- % Identity 90.8
- Alignment Length 185
- Location of Alignment in SEQ ID NO 579: from 1 to 93
  
- Alignment No. 6108
- gi No. 1769905
- % Identity 99.1
- Alignment Length 231
- Location of Alignment in SEQ ID NO 579: from 1 to 93
  
- Alignment No. 6109
- gi No. 1771778
- % Identity 77.4
- Alignment Length 233
- Location of Alignment in SEQ ID NO 579: from 1 to 93
  
- Alignment No. 6110
- gi No. 266856
- % Identity 77.8
- Alignment Length 231
- Location of Alignment in SEQ ID NO 579: from 1 to 93
  
- Alignment No. 6111
- gi No. 2880056
- % Identity 80.5
- Alignment Length 232
- Location of Alignment in SEQ ID NO 579: from 1 to 93

- Alignment No. 6112
- gi No. 2921508
- % Identity 70.3
- Alignment Length 234
- Location of Alignment in SEQ ID NO 579: from 1 to 93
  
- Alignment No. 6113
- gi No. 625545
- % Identity 81.5
- Alignment Length 173
- Location of Alignment in SEQ ID NO 579: from 1 to 93
  
- Alignment No. 6114
- gi No. 625546
- % Identity 77.5
- Alignment Length 238
- Location of Alignment in SEQ ID NO 579: from 1 to 93
  
- Alignment No. 6115
- gi No. 81723
- % Identity 88.1
- Alignment Length 219
- Location of Alignment in SEQ ID NO 579: from 1 to 93
  
- Alignment No. 6116
- gi No. 82188
- % Identity 79
- Alignment Length 229
- Location of Alignment in SEQ ID NO 579: from 1 to 86
  
- Alignment No. 6117
- gi No. 82189
- % Identity 79
- Alignment Length 229
- Location of Alignment in SEQ ID NO 579: from 1 to 93

Maximum Length Sequence corresponding to clone ID 143346

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 580
- Ceres seq\_id 1498665

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 581
- Ceres seq\_id 1498666
- Location of start within SEQ ID NO 580: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6118
- gi No. 2924518
- % Identity 94.6
- Alignment Length 37
- Location of Alignment in SEQ ID NO 581: from 30 to 66

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 582
- Ceres seq\_id 1498667
- Location of start within SEQ ID NO 580: at 89 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 6119
  - gi No. 2924518
  - % Identity 94.6
  - Alignment Length 37
  - Location of Alignment in SEQ ID NO 582: from 1 to 37

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 583
  - Ceres seq\_id 1498668
  - Location of start within SEQ ID NO 580: at 177 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 143795

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 584
- Ceres seq\_id 1498671

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 585
- Ceres seq\_id 1498672
- Location of start within SEQ ID NO 584: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6120
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 585: from 96 to 188 aa.

- (D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 586
- Ceres seq\_id 1498673
- Location of start within SEQ ID NO 584: at 34 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6121
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 586: from 85 to 177 aa.

- (D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 587
- Ceres seq\_id 1498674
- Location of start within SEQ ID NO 584: at 265 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6122
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 587: from 8 to 100 aa.

- (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 144685

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 588
- Ceres seq\_id 1498679
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 589
  - Ceres seq\_id 1498680
  - Location of start within SEQ ID NO 588: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 6123
  - gi No. 4972062
  - % Identity 81.1
  - Alignment Length 37
  - Location of Alignment in SEQ ID NO 589: from 74 to 110

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 590
  - Ceres seq\_id 1498681
  - Location of start within SEQ ID NO 588: at 303 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
  - Alignment No. 6124
  - gi No. 4972062
  - % Identity 75.3
  - Alignment Length 73
  - Location of Alignment in SEQ ID NO 590: from 1 to 52

Maximum Length Sequence corresponding to clone ID 145124

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 591
- Ceres seq\_id 1498682

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 592
- Ceres seq\_id 1498683
- Location of start within SEQ ID NO 591: at 404 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6125
- VHS domain
- Location within SEQ ID NO 592: from 1 to 63 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6126
- gi No. 3063694
- % Identity 100
- Alignment Length 43
- Location of Alignment in SEQ ID NO 592: from 237 to 279

- Alignment No. 6127
- gi No. 3063694
- % Identity 100
- Alignment Length 66
- Location of Alignment in SEQ ID NO 592: from 171 to 236

- Alignment No. 6128
- gi No. 3063694
- % Identity 93.2

- Alignment Length 88
- Location of Alignment in SEQ ID NO 592: from 61 to 148
- Alignment No. 6129
- gi No. 3063694
- % Identity 82
- Alignment Length 89
- Location of Alignment in SEQ ID NO 592: from 1 to 61

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 593
- Ceres seq\_id 1498684
- Location of start within SEQ ID NO 591: at 413 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6130
- VHS domain
- Location within SEQ ID NO 593: from 1 to 60 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6131
- gi No. 3063694
- % Identity 100
- Alignment Length 43
- Location of Alignment in SEQ ID NO 593: from 234 to 276
- Alignment No. 6132
- gi No. 3063694
- % Identity 100
- Alignment Length 66
- Location of Alignment in SEQ ID NO 593: from 168 to 233
- Alignment No. 6133
- gi No. 3063694
- % Identity 93.2
- Alignment Length 88
- Location of Alignment in SEQ ID NO 593: from 58 to 145
- Alignment No. 6134
- gi No. 3063694
- % Identity 82
- Alignment Length 89
- Location of Alignment in SEQ ID NO 593: from 1 to 58

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 594
- Ceres seq\_id 1498685
- Location of start within SEQ ID NO 591: at 446 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6135
- gi No. 3063694
- % Identity 100
- Alignment Length 43
- Location of Alignment in SEQ ID NO 594: from 223 to 265
- Alignment No. 6136
- gi No. 3063694

- % Identity 100
- Alignment Length 66
- Location of Alignment in SEQ ID NO 594: from 157 to 222
  
- Alignment No. 6137
- gi No. 3063694
- % Identity 93.2
- Alignment Length 88
- Location of Alignment in SEQ ID NO 594: from 47 to 134
  
- Alignment No. 6138
- gi No. 3063694
- % Identity 82
- Alignment Length 89
- Location of Alignment in SEQ ID NO 594: from 1 to 47

Maximum Length Sequence corresponding to clone ID 145165

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 595
- Ceres seq\_id 1498686

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 596
- Ceres seq\_id 1498687
- Location of start within SEQ ID NO 595: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6139
- Thioredoxin
- Location within SEQ ID NO 596: from 97 to 183 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6140
- gi No. 3004560
- % Identity 98.6
- Alignment Length 211
- Location of Alignment in SEQ ID NO 596: from 22 to 232

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 597
- Ceres seq\_id 1498688
- Location of start within SEQ ID NO 595: at 64 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6141
- Thioredoxin
- Location within SEQ ID NO 597: from 76 to 162 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6142
- gi No. 3004560
- % Identity 98.6
- Alignment Length 211
- Location of Alignment in SEQ ID NO 597: from 1 to 211

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 598
- Ceres seq\_id 1498689
- Location of start within SEQ ID NO 595: at 121 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6143
- Thioredoxin
- Location within SEQ ID NO 598: from 57 to 143 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6144
- gi No. 3004560
- % Identity 98.6
- Alignment Length 211
- Location of Alignment in SEQ ID NO 598: from 1 to 192

Maximum Length Sequence corresponding to clone ID 146143

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 599
- Ceres seq\_id 1498690

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 600
- Ceres seq\_id 1498691
- Location of start within SEQ ID NO 599: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6145
- gi No. 4567312
- % Identity 98.6
- Alignment Length 357
- Location of Alignment in SEQ ID NO 600: from 116 to 471

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 601
- Ceres seq\_id 1498692
- Location of start within SEQ ID NO 599: at 165 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6146
- gi No. 4567312
- % Identity 98.6
- Alignment Length 357
- Location of Alignment in SEQ ID NO 601: from 62 to 417

Maximum Length Sequence corresponding to clone ID 147552

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 602
- Ceres seq\_id 1498703

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 603
- Ceres seq\_id 1498704
- Location of start within SEQ ID NO 602: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6147
- Uncharacterized protein family UPF0004
- Location within SEQ ID NO 603: from 76 to 497 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 604
- Ceres seq\_id 1498705
- Location of start within SEQ ID NO 602: at 33 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6148
- Uncharacterized protein family UPF0004
- Location within SEQ ID NO 604: from 66 to 487 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 605
- Ceres seq\_id 1498706
- Location of start within SEQ ID NO 602: at 204 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6149
- Uncharacterized protein family UPF0004
- Location within SEQ ID NO 605: from 9 to 430 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 147694

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 606
- Ceres seq\_id 1498718

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 607
- Ceres seq\_id 1498719
- Location of start within SEQ ID NO 606: at 308 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6150
- Leucine Rich Repeat
- Location within SEQ ID NO 607: from 53 to 75 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6151
- gi No. 3687240
- % Identity 74.2
- Alignment Length 407
- Location of Alignment in SEQ ID NO 607: from 1 to 321

Maximum Length Sequence corresponding to clone ID 148127

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 608
- Ceres seq\_id 1498735

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 609
- Ceres seq\_id 1498736
- Location of start within SEQ ID NO 608: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6152



- GDA1/CD39 (nucleoside phosphatase) family
- Location within SEQ ID NO 609: from 167 to 266 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 610
- Ceres seq\_id 1498737
- Location of start within SEQ ID NO 608: at 974 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6153
- GDA1/CD39 (nucleoside phosphatase) family
- Location within SEQ ID NO 610: from 1 to 242 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 611
- Ceres seq\_id 1498738
- Location of start within SEQ ID NO 608: at 1052 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6154
- GDA1/CD39 (nucleoside phosphatase) family
- Location within SEQ ID NO 611: from 1 to 216 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 148308

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 612
- Ceres seq\_id 1498739

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 613
- Ceres seq\_id 1498740
- Location of start within SEQ ID NO 612: at 283 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6155
- gi No. 584350
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 613: from 277 to 297

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 614
- Ceres seq\_id 1498741
- Location of start within SEQ ID NO 612: at 328 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6156
- gi No. 584350
- % Identity 71.4
- Alignment Length 21

- Location of Alignment in SEQ ID NO 614: from 262 to 282

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 615
- Ceres seq\_id 1498742
- Location of start within SEQ ID NO 612: at 520 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6157
- gi No. 584350
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 615: from 198 to 218

Maximum Length Sequence corresponding to clone ID 148366

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 616
- Ceres seq\_id 1498743

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 617
- Ceres seq\_id 1498744
- Location of start within SEQ ID NO 616: at 149 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6158
- tRNA synthetases class II (F)
- Location within SEQ ID NO 617: from 95 to 285 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 618
- Ceres seq\_id 1498745
- Location of start within SEQ ID NO 616: at 278 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6159
- tRNA synthetases class II (F)
- Location within SEQ ID NO 618: from 52 to 242 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 148486

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 619
- Ceres seq\_id 1498746

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 620
- Ceres seq\_id 1498747
- Location of start within SEQ ID NO 619: at 153 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6160
- Fatty acid desaturase
- Location within SEQ ID NO 620: from 24 to 382 aa.

|  | 1970 | 1971 | 1972 | 1973 | 1974 | 1975 | 1976 | 1977 | 1978 | 1979 | 1980 | 1981 | 1982 | 1983 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 | 2101 | 2102 | 2103 | 2104 | 2105 | 2106 | 2107 | 2108 | 2109 | 2110 | 2111 | 2112 | 2113 | 2114 | 2115 | 2116 | 2117 | 2118 | 2119 | 2120 | 2121 | 2122 | 2123 | 2124 | 2125 | 2126 | 2127 | 2128 | 2129 | 2130 | 2131 | 2132 | 2133 | 2134 | 2135 | 2136 | 2137 | 2138 | 2139 | 2140 | 2141 | 2142 | 2143 | 2144 | 2145 | 2146 | 2147 | 2148 | 2149 | 2150 | 2151 | 2152 | 2153 | 2154 | 2155 | 2156 | 2157 | 2158 | 2159 | 2160 | 2161 | 2162 | 2163 | 2164 | 2165 | 2166 | 2167 | 2168 | 2169 | 2170 | 2171 | 2172 | 2173 | 2174 | 2175 | 2176 | 2177 | 2178 | 2179 | 2180 | 2181 | 2182 | 2183 | 2184 | 2185 | 2186 | 2187 | 2188 | 2189 | 2190 | 2191 | 2192 | 2193 | 2194 | 2195 | 2196 | 2197 | 2198 | 2199 | 2200 | 2201 | 2202 | 2203 | 2204 | 2205 | 2206 | 2207 | 2208 | 2209 | 2210 | 2211 | 2212 | 2213 | 2214 | 2215 | 2216 | 2217 | 2218 | 2219 | 2220 | 2221 | 2222 | 2223 | 2224 | 2225 | 2226 | 2227 | 2228 | 2229 | 2230 | 2231 | 2232 | 2233 | 2234 | 2235 | 2236 | 2237 | 2238 | 2239 | 2240 | 2241 | 2242 | 2243 | 2244 | 2245 | 2246 | 2247 | 2248 | 2249 | 2250 | 2251 | 2252 | 2253 | 2254 | 2255 | 2256 | 2257 | 2258 | 2259 | 2260 | 2261 | 2262 | 2263 | 2264 | 2265 | 2266 | 2267 | 2268 | 2269 | 2270 | 2271 | 2272 | 2273 | 2274 | 2275 | 2276 | 2277 | 2278 | 2279 | 2280 | 2281 | 2282 | 2283 | 2284 | 2285 | 2286 | 2287 | 2288 | 2289 | 2290 | 2291 | 2292 | 2293 | 2294 | 2295 | 2296 | 2297 | 2298 | 2299 | 2300 | 2301 | 2302 | 2303 | 2304 | 2305 | 2306 | 2307 | 2308 | 2309 | 2310 | 2311 | 2312 | 2313 | 2314 | 2315 | 2316 | 2317 | 2318 | 2319 | 2320 | 2321 | 2322 | 2323 | 2324 | 2325 | 2326 | 2327 | 2328 | 2329 | 2330 | 2331 | 2332 | 2333 | 2334 | 2335 | 2336 | 2337 | 2338 | 2339 | 2340 | 2341 | 2342 | 2343 | 2344 | 2345 | 2346 | 2347 | 2348 | 2349 | 2350 | 2351 | 2352 | 2353 | 2354 | 2355 | 2356 | 2357 | 2358 | 2359 | 2360 | 2361 | 2362 | 2363 | 2364 | 2365 | 2366 | 2367 | 2368 | 2369 | 2370 | 2371 | 2372 | 2373 | 2374 | 2375 | 2376 | 2377 | 2378 | 2379 | 2380 | 2381 | 2382 | 2383 | 2384 | 2385 | 2386 | 2387 | 2388 | 2389 | 2390 | 2391 | 2392 | 2393 | 2394 | 2395 | 2396 | 2397 | 2398 | 2399 | 2400 | 2401 | 2402 | 2403 | 2404 | 2405 | 2406 | 2407 | 2408 | 2409 | 2410 | 2411 | 2412 | 2413 | 2414 | 2415 | 2416 | 2417 | 2418 | 2419 | 2420 | 2421 | 2422 | 2 |
|--|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|---|
|--|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|---|

- Alignment No. 6161
- gi No. 1054843
- % Identity 74.2
- Alignment Length 383
- Location of Alignment in SEQ ID NO 620: from 1 to 383
- Alignment No. 6162
- gi No. 1169598
- % Identity 100
- Alignment Length 383
- Location of Alignment in SEQ ID NO 620: from 1 to 383
- Alignment No. 6163
- gi No. 1345977
- % Identity 76.2
- Alignment Length 383
- Location of Alignment in SEQ ID NO 620: from 1 to 383
- Alignment No. 6164
- gi No. 2501790
- % Identity 75.2
- Alignment Length 384
- Location of Alignment in SEQ ID NO 620: from 1 to 383
- Alignment No. 6165
- gi No. 2564237
- % Identity 76.8
- Alignment Length 384
- Location of Alignment in SEQ ID NO 620: from 1 to 383
- Alignment No. 6166
- gi No. 2578033
- % Identity 71.6
- Alignment Length 385
- Location of Alignment in SEQ ID NO 620: from 1 to 382
- Alignment No. 6167
- gi No. 2613051
- % Identity 70.7
- Alignment Length 382
- Location of Alignment in SEQ ID NO 620: from 1 to 382
- Alignment No. 6168
- gi No. 3135020
- % Identity 74.4
- Alignment Length 383
- Location of Alignment in SEQ ID NO 620: from 1 to 383
- Alignment No. 6169
- gi No. 3264765
- % Identity 79.3
- Alignment Length 347
- Location of Alignment in SEQ ID NO 620: from 37 to 383
- Alignment No. 6170
- gi No. 3334184
- % Identity 90.4
- Alignment Length 384
- Location of Alignment in SEQ ID NO 620: from 1 to 383

- Alignment No. 6171
- gi No. 3417601
- % Identity 77.8
- Alignment Length 384
- Location of Alignment in SEQ ID NO 620: from 1 to 383
  
- Alignment No. 6172
- gi No. 3452129
- % Identity 84.9
- Alignment Length 384
- Location of Alignment in SEQ ID NO 620: from 1 to 383
  
- Alignment No. 6173
- gi No. 3452132
- % Identity 83.4
- Alignment Length 181
- Location of Alignment in SEQ ID NO 620: from 139 to 319
  
- Alignment No. 6174
- gi No. 3452135
- % Identity 92.5
- Alignment Length 161
- Location of Alignment in SEQ ID NO 620: from 139 to 299
  
- Alignment No. 6175
- gi No. 4092879
- % Identity 91.7
- Alignment Length 312
- Location of Alignment in SEQ ID NO 620: from 57 to 367
  
- Alignment No. 6176
- gi No. 4378875
- % Identity 91.1
- Alignment Length 384
- Location of Alignment in SEQ ID NO 620: from 1 to 383

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 621
- Ceres seq\_id 1498748
- Location of start within SEQ ID NO 619: at 171 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6177
- Fatty acid desaturase
- Location within SEQ ID NO 621: from 18 to 376 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6178
- gi No. 1054843
- % Identity 74.2
- Alignment Length 383
- Location of Alignment in SEQ ID NO 621: from 1 to 377
  
- Alignment No. 6179
- gi No. 1169598
- % Identity 100
- Alignment Length 383
- Location of Alignment in SEQ ID NO 621: from 1 to 377
  
- Alignment No. 6180

- gi No. 1345977
- % Identity 76.2
- Alignment Length 383
- Location of Alignment in SEQ ID NO 621: from 1 to 377
  
- Alignment No. 6181
- gi No. 2501790
- % Identity 75.2
- Alignment Length 384
- Location of Alignment in SEQ ID NO 621: from 1 to 377
  
- Alignment No. 6182
- gi No. 2564237
- % Identity 76.8
- Alignment Length 384
- Location of Alignment in SEQ ID NO 621: from 1 to 377
  
- Alignment No. 6183
- gi No. 2578033
- % Identity 71.6
- Alignment Length 385
- Location of Alignment in SEQ ID NO 621: from 1 to 376
  
- Alignment No. 6184
- gi No. 2613051
- % Identity 70.7
- Alignment Length 382
- Location of Alignment in SEQ ID NO 621: from 1 to 376
  
- Alignment No. 6185
- gi No. 3135020
- % Identity 74.4
- Alignment Length 383
- Location of Alignment in SEQ ID NO 621: from 1 to 377
  
- Alignment No. 6186
- gi No. 3264765
- % Identity 79.3
- Alignment Length 347
- Location of Alignment in SEQ ID NO 621: from 31 to 377
  
- Alignment No. 6187
- gi No. 3334184
- % Identity 90.4
- Alignment Length 384
- Location of Alignment in SEQ ID NO 621: from 1 to 377
  
- Alignment No. 6188
- gi No. 3417601
- % Identity 77.8
- Alignment Length 384
- Location of Alignment in SEQ ID NO 621: from 1 to 377
  
- Alignment No. 6189
- gi No. 3452129
- % Identity 84.9
- Alignment Length 384
- Location of Alignment in SEQ ID NO 621: from 1 to 377
  
- Alignment No. 6190
- gi No. 3452132

- % Identity 83.4
- Alignment Length 181
- Location of Alignment in SEQ ID NO 621: from 133 to 313
  
- Alignment No. 6191
- gi No. 3452135
- % Identity 92.5
- Alignment Length 161
- Location of Alignment in SEQ ID NO 621: from 133 to 293
  
- Alignment No. 6192
- gi No. 4092879
- % Identity 91.7
- Alignment Length 312
- Location of Alignment in SEQ ID NO 621: from 51 to 361
  
- Alignment No. 6193
- gi No. 4378875
- % Identity 91.1
- Alignment Length 384
- Location of Alignment in SEQ ID NO 621: from 1 to 377

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 622
- Ceres seq\_id 1498749
- Location of start within SEQ ID NO 619: at 690 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6194
- Fatty acid desaturase
- Location within SEQ ID NO 622: from 1 to 203 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6195
- gi No. 1054843
- % Identity 74.2
- Alignment Length 383
- Location of Alignment in SEQ ID NO 622: from 1 to 204
  
- Alignment No. 6196
- gi No. 1169598
- % Identity 100
- Alignment Length 383
- Location of Alignment in SEQ ID NO 622: from 1 to 204
  
- Alignment No. 6197
- gi No. 1345977
- % Identity 76.2
- Alignment Length 383
- Location of Alignment in SEQ ID NO 622: from 1 to 204
  
- Alignment No. 6198
- gi No. 2501790
- % Identity 75.2
- Alignment Length 384
- Location of Alignment in SEQ ID NO 622: from 1 to 204
  
- Alignment No. 6199
- gi No. 2564237
- % Identity 76.8

- Alignment Length 384
- Location of Alignment in SEQ ID NO 622: from 1 to 204
- Alignment No. 6200
- gi No. 2578033
- % Identity 71.6
- Alignment Length 385
- Location of Alignment in SEQ ID NO 622: from 1 to 203
- Alignment No. 6201
- gi No. 2613051
- % Identity 70.7
- Alignment Length 382
- Location of Alignment in SEQ ID NO 622: from 1 to 203
- Alignment No. 6202
- gi No. 3135020
- % Identity 74.4
- Alignment Length 383
- Location of Alignment in SEQ ID NO 622: from 1 to 204
- Alignment No. 6203
- gi No. 3264765
- % Identity 79.3
- Alignment Length 347
- Location of Alignment in SEQ ID NO 622: from 1 to 204
- Alignment No. 6204
- gi No. 3334184
- % Identity 90.4
- Alignment Length 384
- Location of Alignment in SEQ ID NO 622: from 1 to 204
- Alignment No. 6205
- gi No. 3417601
- % Identity 77.8
- Alignment Length 384
- Location of Alignment in SEQ ID NO 622: from 1 to 204
- Alignment No. 6206
- gi No. 3452129
- % Identity 84.9
- Alignment Length 384
- Location of Alignment in SEQ ID NO 622: from 1 to 204
- Alignment No. 6207
- gi No. 3452132
- % Identity 83.4
- Alignment Length 181
- Location of Alignment in SEQ ID NO 622: from 1 to 140
- Alignment No. 6208
- gi No. 3452135
- % Identity 92.5
- Alignment Length 161
- Location of Alignment in SEQ ID NO 622: from 1 to 120
- Alignment No. 6209
- gi No. 4092879
- % Identity 91.7
- Alignment Length 312

- Location of Alignment in SEQ ID NO 622: from 1 to 188
- Alignment No. 6210
- gi No. 4378875
- % Identity 91.1
- Alignment Length 384
- Location of Alignment in SEQ ID NO 622: from 1 to 204

Maximum Length Sequence corresponding to clone ID 148506

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 623
- Ceres seq\_id 1498750

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 624
- Ceres seq\_id 1498751
- Location of start within SEQ ID NO 623: at 198 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6211
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 624: from 150 to 220 aa.
- Alignment No. 6212
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 624: from 271 to 338 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6213
- gi No. 2565067
- % Identity 84.6
- Alignment Length 13
- Location of Alignment in SEQ ID NO 624: from 8 to 20
- Alignment No. 6214
- gi No. 2565067
- % Identity 84.6
- Alignment Length 13
- Location of Alignment in SEQ ID NO 624: from 8 to 20
- Alignment No. 6215
- gi No. 2565067
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 624: from 8 to 20
- Alignment No. 6216
- gi No. 2565067
- % Identity 84.6
- Alignment Length 13
- Location of Alignment in SEQ ID NO 624: from 8 to 20
- Alignment No. 6217
- gi No. 4587549
- % Identity 99.5
- Alignment Length 426
- Location of Alignment in SEQ ID NO 624: from 1 to 426

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 625
- Ceres seq\_id 1498752



- Location of start within SEQ ID NO 623: at 261 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6218
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 625: from 129 to 199 aa.
- Alignment No. 6219
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 625: from 250 to 317 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6220
- gi No. 4587549
- % Identity 99.5
- Alignment Length 426
- Location of Alignment in SEQ ID NO 625: from 1 to 405

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 626
- Ceres seq\_id 1498753
- Location of start within SEQ ID NO 623: at 276 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6221
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 626: from 124 to 194 aa.
- Alignment No. 6222
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 626: from 245 to 312 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6223
- gi No. 4587549
- % Identity 99.5
- Alignment Length 426
- Location of Alignment in SEQ ID NO 626: from 1 to 400

Maximum Length Sequence corresponding to clone ID 148728

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 627
- Ceres seq\_id 1498754

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 628
- Ceres seq\_id 1498755
- Location of start within SEQ ID NO 627: at 58 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6224
- Lipoprotein amino terminal region
- Location within SEQ ID NO 628: from 81 to 254 aa.
- Alignment No. 6225
- Granin (chromogranin or secretogranin)
- Location within SEQ ID NO 628: from 25 to 246 aa.
- Alignment No. 6226

- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 628: from 22 to 194 aa.
- Alignment No. 6227
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 628: from 29 to 241 aa.
- Alignment No. 6228
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 628: from 68 to 241 aa.
- Alignment No. 6229
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 628: from 81 to 248 aa.
- Alignment No. 6230
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 628: from 88 to 248 aa.
- Alignment No. 6231
- 11-S plant seed storage protein
- Location within SEQ ID NO 628: from 24 to 214 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6232
- gi No. 2262136
- % Identity 99.6
- Alignment Length 249
- Location of Alignment in SEQ ID NO 628: from 3 to 251

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 629
- Ceres seq\_id 1498756
- Location of start within SEQ ID NO 627: at 64 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6233
- Lipoprotein amino terminal region
- Location within SEQ ID NO 629: from 79 to 252 aa.
- Alignment No. 6234
- Granin (chromogranin or secretogranin)
- Location within SEQ ID NO 629: from 23 to 244 aa.
- Alignment No. 6235
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 629: from 20 to 192 aa.
- Alignment No. 6236
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 629: from 27 to 239 aa.
- Alignment No. 6237
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 629: from 66 to 239 aa.
- Alignment No. 6238
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 629: from 79 to 246 aa.

- Alignment No. 6239
  - Eukaryotic DNA topoisomerase I
  - Location within SEQ ID NO 629: from 86 to 246 aa.
- 
- Alignment No. 6240
  - 11-S plant seed storage protein
  - Location within SEQ ID NO 629: from 22 to 212 aa.

#### (D) Related Amino Acid Sequences

- ```
- Alignment No. 6241
- gi No. 2262136
- % Identity 99.6
- Alignment Length 249
- Location of Alignment in SEQ ID NO 629: from 1 to 249
```

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 630
- Ceres seq_id 1498757
- Location of start within SEQ ID NO 627: at 208 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6242
- Lipoprotein amino terminal region
- Location within SEQ ID NO 630: from 31 to 204 aa.
- Alignment No. 6243
- Granin (chromogranin or secretogranin)
- Location within SEQ ID NO 630: from 1 to 196 aa.
- Alignment No. 6244
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 630: from 1 to 144 aa.
- Alignment No. 6245
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 630: from 1 to 191 aa.
- Alignment No. 6246
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 630: from 18 to 191 aa.
- Alignment No. 6247
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 630: from 31 to 198 aa.
- Alignment No. 6248
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 630: from 38 to 198 aa.
- Alignment No. 6249
- 11-S plant seed storage protein
- Location within SEQ ID NO 630: from 1 to 164 aa.

(D) Related Amino Acid Sequences

- ```
- Alignment No. 6250
- gi No. 2262136
- % Identity 99.6
- Alignment Length 249
- Location of Alignment in SEQ ID NO 630: from 1 to 201
```

Maximum Length Sequence corresponding to clone ID 149067

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 631
- Ceres seq\_id 1498758

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 632
- Ceres seq\_id 1498759
- Location of start within SEQ ID NO 631: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6251
- Oxidoreductase FAD/NAD-binding domain
- Location within SEQ ID NO 632: from 208 to 302 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6252
- gi No. 1065268
- % Identity 85.9
- Alignment Length 256
- Location of Alignment in SEQ ID NO 632: from 49 to 301
- Alignment No. 6253
- gi No. 1065318
- % Identity 85.5
- Alignment Length 256
- Location of Alignment in SEQ ID NO 632: from 49 to 301
- Alignment No. 6254
- gi No. 119905
- % Identity 81.8
- Alignment Length 306
- Location of Alignment in SEQ ID NO 632: from 1 to 302
- Alignment No. 6255
- gi No. 119906
- % Identity 78.1
- Alignment Length 311
- Location of Alignment in SEQ ID NO 632: from 1 to 301
- Alignment No. 6256
- gi No. 1375093
- % Identity 88.9
- Alignment Length 27
- Location of Alignment in SEQ ID NO 632: from 270 to 296
- Alignment No. 6257
- gi No. 170111
- % Identity 78.1
- Alignment Length 311
- Location of Alignment in SEQ ID NO 632: from 1 to 301
- Alignment No. 6258
- gi No. 294092
- % Identity 87.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 632: from 270 to 302
- Alignment No. 6259
- gi No. 294095
- % Identity 87.9

- Alignment Length 33
- Location of Alignment in SEQ ID NO 632: from 270 to 302
  
- Alignment No. 6260
- gi No. 294097
- % Identity 87.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 632: from 270 to 302
  
- Alignment No. 6261
- gi No. 3088648
- % Identity 90.6
- Alignment Length 32
- Location of Alignment in SEQ ID NO 632: from 155 to 186
  
- Alignment No. 6262
- gi No. 3088650
- % Identity 88.9
- Alignment Length 27
- Location of Alignment in SEQ ID NO 632: from 153 to 179
  
- Alignment No. 6263
- gi No. 3088652
- % Identity 90
- Alignment Length 30
- Location of Alignment in SEQ ID NO 632: from 151 to 180
  
- Alignment No. 6264
- gi No. 3088654
- % Identity 91.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 632: from 146 to 180
  
- Alignment No. 6265
- gi No. 3891912
- % Identity 85.9
- Alignment Length 256
- Location of Alignment in SEQ ID NO 632: from 49 to 301
  
- Alignment No. 6266
- gi No. 3891918
- % Identity 85.9
- Alignment Length 256
- Location of Alignment in SEQ ID NO 632: from 49 to 301
  
- Alignment No. 6267
- gi No. 3891919
- % Identity 85.9
- Alignment Length 256
- Location of Alignment in SEQ ID NO 632: from 49 to 301
  
- Alignment No. 6268
- gi No. 3913651
- % Identity 80.3
- Alignment Length 308
- Location of Alignment in SEQ ID NO 632: from 1 to 302
  
- Alignment No. 6269
- gi No. 4930119
- % Identity 90
- Alignment Length 249

- Location of Alignment in SEQ ID NO 632: from 54 to 302
- Alignment No. 6270
- gi No. 4930123
- % Identity 90
- Alignment Length 249
- Location of Alignment in SEQ ID NO 632: from 54 to 302
- Alignment No. 6271
- gi No. 4930128
- % Identity 90
- Alignment Length 249
- Location of Alignment in SEQ ID NO 632: from 54 to 302
- Alignment No. 6272
- gi No. 729477
- % Identity 79.3
- Alignment Length 306
- Location of Alignment in SEQ ID NO 632: from 1 to 300
- Alignment No. 6273
- gi No. 729478
- % Identity 74.3
- Alignment Length 308
- Location of Alignment in SEQ ID NO 632: from 1 to 302
- Alignment No. 6274
- gi No. 729479
- % Identity 82.6
- Alignment Length 306
- Location of Alignment in SEQ ID NO 632: from 1 to 302

Maximum Length Sequence corresponding to clone ID 149102

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 633
- Ceres seq\_id 1498760

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 634
- Ceres seq\_id 1498761
- Location of start within SEQ ID NO 633: at 569 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6275
- gi No. 2388580
- % Identity 78.7
- Alignment Length 333
- Location of Alignment in SEQ ID NO 634: from 1 to 289
- Alignment No. 6276
- gi No. 3831453
- % Identity 76
- Alignment Length 339
- Location of Alignment in SEQ ID NO 634: from 1 to 289
- Alignment No. 6277
- gi No. 4455217
- % Identity 100
- Alignment Length 332
- Location of Alignment in SEQ ID NO 634: from 1 to 289

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 635
- Ceres seq\_id 1498762
- Location of start within SEQ ID NO 633: at 635 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6278
- gi No. 2388580
- % Identity 78.7
- Alignment Length 333
- Location of Alignment in SEQ ID NO 635: from 1 to 267
- Alignment No. 6279
- gi No. 3831453
- % Identity 76
- Alignment Length 339
- Location of Alignment in SEQ ID NO 635: from 1 to 267
- Alignment No. 6280
- gi No. 4455217
- % Identity 100
- Alignment Length 332
- Location of Alignment in SEQ ID NO 635: from 1 to 267

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 636
- Ceres seq\_id 1498763
- Location of start within SEQ ID NO 633: at 701 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6281
- gi No. 2388580
- % Identity 78.7
- Alignment Length 333
- Location of Alignment in SEQ ID NO 636: from 1 to 245
- Alignment No. 6282
- gi No. 3831453
- % Identity 76
- Alignment Length 339
- Location of Alignment in SEQ ID NO 636: from 1 to 245
- Alignment No. 6283
- gi No. 4455217
- % Identity 100
- Alignment Length 332
- Location of Alignment in SEQ ID NO 636: from 1 to 245

Maximum Length Sequence corresponding to clone ID 149202

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 637
- Ceres seq\_id 1498764

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 638
- Ceres seq\_id 1498765
- Location of start within SEQ ID NO 637: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6284
- gi No. 100454
- % Identity 83.2
- Alignment Length 167
- Location of Alignment in SEQ ID NO 638: from 102 to 266
  
- Alignment No. 6285
- gi No. 131381
- % Identity 74.1
- Alignment Length 161
- Location of Alignment in SEQ ID NO 638: from 12 to 161
  
- Alignment No. 6286
- gi No. 131381
- % Identity 98.2
- Alignment Length 167
- Location of Alignment in SEQ ID NO 638: from 102 to 266
  
- Alignment No. 6287
- gi No. 131383
- % Identity 85.4
- Alignment Length 41
- Location of Alignment in SEQ ID NO 638: from 226 to 266
  
- Alignment No. 6288
- gi No. 131384
- % Identity 84.4
- Alignment Length 167
- Location of Alignment in SEQ ID NO 638: from 102 to 266
  
- Alignment No. 6289
- gi No. 131385
- % Identity 83.2
- Alignment Length 167
- Location of Alignment in SEQ ID NO 638: from 102 to 266
  
- Alignment No. 6290
- gi No. 131386
- % Identity 85.6
- Alignment Length 167
- Location of Alignment in SEQ ID NO 638: from 102 to 266
  
- Alignment No. 6291
- gi No. 131388
- % Identity 80
- Alignment Length 167
- Location of Alignment in SEQ ID NO 638: from 102 to 266
  
- Alignment No. 6292
- gi No. 19157
- % Identity 85.6
- Alignment Length 167
- Location of Alignment in SEQ ID NO 638: from 102 to 266
  
- Alignment No. 6293
- gi No. 2921506
- % Identity 83.2

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- Alignment Length 167
- Location of Alignment in SEQ ID NO 638: from 102 to 266
  
- Alignment No. 6294
- gi No. 3286693
- % Identity 74.1
- Alignment Length 161
- Location of Alignment in SEQ ID NO 638: from 12 to 161
  
- Alignment No. 6295
- gi No. 3286693
- % Identity 98.2
- Alignment Length 167
- Location of Alignment in SEQ ID NO 638: from 102 to 266
  
- Alignment No. 6296
- gi No. 4006857
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 638: from 103 to 114
  
- Alignment No. 6297
- gi No. 482311
- % Identity 85
- Alignment Length 167
- Location of Alignment in SEQ ID NO 638: from 102 to 266
  
- Alignment No. 6298
- gi No. 4835233
- % Identity 93.4
- Alignment Length 167
- Location of Alignment in SEQ ID NO 638: from 102 to 266
  
- Alignment No. 6299
- gi No. 505482
- % Identity 86.2
- Alignment Length 167
- Location of Alignment in SEQ ID NO 638: from 102 to 266
  
- Alignment No. 6300
- gi No. 81454
- % Identity 85.6
- Alignment Length 167
- Location of Alignment in SEQ ID NO 638: from 102 to 266
  
- Alignment No. 6301
- gi No. 81478
- % Identity 85.6
- Alignment Length 167
- Location of Alignment in SEQ ID NO 638: from 102 to 266

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 639
- Ceres seq\_id 1498766
- Location of start within SEQ ID NO 637: at 35 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6302
- gi No. 100454

- % Identity 83.2
- Alignment Length 167
- Location of Alignment in SEQ ID NO 639: from 91 to 255
  
- Alignment No. 6303
- gi No. 131381
- % Identity 74.1
- Alignment Length 161
- Location of Alignment in SEQ ID NO 639: from 1 to 150
  
- Alignment No. 6304
- gi No. 131381
- % Identity 98.2
- Alignment Length 167
- Location of Alignment in SEQ ID NO 639: from 91 to 255
  
- Alignment No. 6305
- gi No. 131383
- % Identity 85.4
- Alignment Length 41
- Location of Alignment in SEQ ID NO 639: from 215 to 255
  
- Alignment No. 6306
- gi No. 131384
- % Identity 84.4
- Alignment Length 167
- Location of Alignment in SEQ ID NO 639: from 91 to 255
  
- Alignment No. 6307
- gi No. 131385
- % Identity 83.2
- Alignment Length 167
- Location of Alignment in SEQ ID NO 639: from 91 to 255
  
- Alignment No. 6308
- gi No. 131386
- % Identity 85.6
- Alignment Length 167
- Location of Alignment in SEQ ID NO 639: from 91 to 255
  
- Alignment No. 6309
- gi No. 131388
- % Identity 80
- Alignment Length 167
- Location of Alignment in SEQ ID NO 639: from 91 to 255
  
- Alignment No. 6310
- gi No. 19157
- % Identity 85.6
- Alignment Length 167
- Location of Alignment in SEQ ID NO 639: from 91 to 255
  
- Alignment No. 6311
- gi No. 2921506
- % Identity 83.2
- Alignment Length 167
- Location of Alignment in SEQ ID NO 639: from 91 to 255
  
- Alignment No. 6312
- gi No. 3286693
- % Identity 74.1

- Alignment Length 161
- Location of Alignment in SEQ ID NO 639: from 1 to 150
  
- Alignment No. 6313
- gi No. 3286693
- % Identity 98.2
- Alignment Length 167
- Location of Alignment in SEQ ID NO 639: from 91 to 255
  
- Alignment No. 6314
- gi No. 4006857
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 639: from 92 to 103
  
- Alignment No. 6315
- gi No. 482311
- % Identity 85
- Alignment Length 167
- Location of Alignment in SEQ ID NO 639: from 91 to 255
  
- Alignment No. 6316
- gi No. 4835233
- % Identity 93.4
- Alignment Length 167
- Location of Alignment in SEQ ID NO 639: from 91 to 255
  
- Alignment No. 6317
- gi No. 505482
- % Identity 86.2
- Alignment Length 167
- Location of Alignment in SEQ ID NO 639: from 91 to 255
  
- Alignment No. 6318
- gi No. 81454
- % Identity 85.6
- Alignment Length 167
- Location of Alignment in SEQ ID NO 639: from 91 to 255
  
- Alignment No. 6319
- gi No. 81478
- % Identity 85.6
- Alignment Length 167
- Location of Alignment in SEQ ID NO 639: from 91 to 255

Maximum Length Sequence corresponding to clone ID 149290

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 640
- Ceres seq\_id 1498771

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 641
- Ceres seq\_id 1498772
- Location of start within SEQ ID NO 640: at 576 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6320
- Proteasome A-type and B-type
- Location within SEQ ID NO 641: from 33 to 107 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6321
- gi No. 1709761
- % Identity 87.6
- Alignment Length 250
- Location of Alignment in SEQ ID NO 641: from 1 to 107
  
- Alignment No. 6322
- gi No. 2244874
- % Identity 100
- Alignment Length 41
- Location of Alignment in SEQ ID NO 641: from 38 to 78
  
- Alignment No. 6323
- gi No. 2511584
- % Identity 92.8
- Alignment Length 250
- Location of Alignment in SEQ ID NO 641: from 1 to 107
  
- Alignment No. 6324
- gi No. 3421077
- % Identity 93.2
- Alignment Length 250
- Location of Alignment in SEQ ID NO 641: from 1 to 107
  
- Alignment No. 6325
- gi No. 3608483
- % Identity 84.8
- Alignment Length 250
- Location of Alignment in SEQ ID NO 641: from 1 to 107
  
- Alignment No. 6326
- gi No. 5091520
- % Identity 81.1
- Alignment Length 249
- Location of Alignment in SEQ ID NO 641: from 1 to 107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 642
- Ceres seq\_id 1498773
- Location of start within SEQ ID NO 640: at 648 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6327
- Proteasome A-type and B-type
- Location within SEQ ID NO 642: from 9 to 83 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6328
- gi No. 1709761
- % Identity 87.6
- Alignment Length 250
- Location of Alignment in SEQ ID NO 642: from 1 to 83
  
- Alignment No. 6329
- gi No. 2244874
- % Identity 100
- Alignment Length 41
- Location of Alignment in SEQ ID NO 642: from 14 to 54
  
- Alignment No. 6330

- gi No. 2511584
- % Identity 92.8
- Alignment Length 250
- Location of Alignment in SEQ ID NO 642: from 1 to 83
  
- Alignment No. 6331
- gi No. 3421077
- % Identity 93.2
- Alignment Length 250
- Location of Alignment in SEQ ID NO 642: from 1 to 83
  
- Alignment No. 6332
- gi No. 3608483
- % Identity 84.8
- Alignment Length 250
- Location of Alignment in SEQ ID NO 642: from 1 to 83
  
- Alignment No. 6333
- gi No. 5091520
- % Identity 81.1
- Alignment Length 249
- Location of Alignment in SEQ ID NO 642: from 1 to 83

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 643
- Ceres seq\_id 1498774
- Location of start within SEQ ID NO 640: at 1020 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6334
- gi No. 1524178
- % Identity 77.8
- Alignment Length 99
- Location of Alignment in SEQ ID NO 643: from 3 to 101
  
- Alignment No. 6335
- gi No. 1709761
- % Identity 87.6
- Alignment Length 250
- Location of Alignment in SEQ ID NO 643: from 1 to 102
  
- Alignment No. 6336
- gi No. 2244874
- % Identity 94.2
- Alignment Length 69
- Location of Alignment in SEQ ID NO 643: from 1 to 52
  
- Alignment No. 6337
- gi No. 2511584
- % Identity 92.8
- Alignment Length 250
- Location of Alignment in SEQ ID NO 643: from 1 to 102
  
- Alignment No. 6338
- gi No. 3421077
- % Identity 93.2
- Alignment Length 250
- Location of Alignment in SEQ ID NO 643: from 1 to 102

- Alignment No. 6339
- gi No. 3608483
- % Identity 84.8
- Alignment Length 250
- Location of Alignment in SEQ ID NO 643: from 1 to 102
  
- Alignment No. 6340
- gi No. 5091520
- % Identity 81.1
- Alignment Length 249
- Location of Alignment in SEQ ID NO 643: from 1 to 100

Maximum Length Sequence corresponding to clone ID 149450

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 644
- Ceres seq\_id 1498775

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 645
- Ceres seq\_id 1498776
- Location of start within SEQ ID NO 644: at 77 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6341
- gi No. 2828295
- % Identity 71.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 645: from 204 to 230
  
- Alignment No. 6342
- gi No. 2828295
- % Identity 70
- Alignment Length 31
- Location of Alignment in SEQ ID NO 645: from 204 to 230
  
- Alignment No. 6343
- gi No. 3451072
- % Identity 75.3
- Alignment Length 158
- Location of Alignment in SEQ ID NO 645: from 5 to 162

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 646
- Ceres seq\_id 1498777
- Location of start within SEQ ID NO 644: at 107 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6344
- gi No. 2828295
- % Identity 71.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 646: from 194 to 220
  
- Alignment No. 6345
- gi No. 2828295
- % Identity 70
- Alignment Length 31
- Location of Alignment in SEQ ID NO 646: from 194 to 220

- Alignment No. 6346
- gi No. 3451072
- % Identity 75.3
- Alignment Length 158
- Location of Alignment in SEQ ID NO 646: from 1 to 152

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 647
- Ceres seq\_id 1498778
- Location of start within SEQ ID NO 644: at 152 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6347
- gi No. 2828295
- % Identity 71.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 647: from 179 to 205
- Alignment No. 6348
- gi No. 2828295
- % Identity 70
- Alignment Length 31
- Location of Alignment in SEQ ID NO 647: from 179 to 205
- Alignment No. 6349
- gi No. 3451072
- % Identity 75.3
- Alignment Length 158
- Location of Alignment in SEQ ID NO 647: from 1 to 137

Maximum Length Sequence corresponding to clone ID 149501

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 648
- Ceres seq\_id 1498779

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 649
- Ceres seq\_id 1498780
- Location of start within SEQ ID NO 648: at 120 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6350
- gi No. 3549679
- % Identity 90
- Alignment Length 110
- Location of Alignment in SEQ ID NO 649: from 12 to 121

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 650
- Ceres seq\_id 1498781
- Location of start within SEQ ID NO 648: at 611 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6351
- gi No. 3549679

2750-1097P-80143.003

- % Identity 98.6
- Alignment Length 147
- Location of Alignment in SEQ ID NO 650: from 1 to 104

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 651
- Ceres seq\_id 1498782
- Location of start within SEQ ID NO 648: at 650 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6352
- gi No. 3549679
- % Identity 98.6
- Alignment Length 147
- Location of Alignment in SEQ ID NO 651: from 1 to 91

Maximum Length Sequence corresponding to clone ID 149654

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 652
- Ceres seq\_id 1498783

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 653
- Ceres seq\_id 1498784
- Location of start within SEQ ID NO 652: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6353
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 653: from 3 to 159 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 654
- Ceres seq\_id 1498785
- Location of start within SEQ ID NO 652: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6354
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 654: from 1 to 124 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 655
- Ceres seq\_id 1498786
- Location of start within SEQ ID NO 652: at 139 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6355
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 655: from 1 to 113 aa.

(D) Related Amino Acid Sequences

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Maximum Length Sequence corresponding to clone ID 150163

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 656
- Ceres seq\_id 1498789

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 657
- Ceres seq\_id 1498790
- Location of start within SEQ ID NO 656: at 306 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6356
- gi No. 4432845
- % Identity 70.8
- Alignment Length 130
- Location of Alignment in SEQ ID NO 657: from 1 to 130
- Alignment No. 6357
- gi No. 4803951
- % Identity 82.7
- Alignment Length 220
- Location of Alignment in SEQ ID NO 657: from 4 to 217

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 658
- Ceres seq\_id 1498791
- Location of start within SEQ ID NO 656: at 315 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6358
- gi No. 4432845
- % Identity 70.8
- Alignment Length 130
- Location of Alignment in SEQ ID NO 658: from 1 to 127
- Alignment No. 6359
- gi No. 4803951
- % Identity 82.7
- Alignment Length 220
- Location of Alignment in SEQ ID NO 658: from 1 to 214

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 659
- Ceres seq\_id 1498792
- Location of start within SEQ ID NO 656: at 459 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6360
- gi No. 4432845
- % Identity 70.8
- Alignment Length 130
- Location of Alignment in SEQ ID NO 659: from 1 to 79
- Alignment No. 6361
- gi No. 4803951
- % Identity 82.7

- Alignment Length 220
- Location of Alignment in SEQ ID NO 659: from 1 to 166

Maximum Length Sequence corresponding to clone ID 150522

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 660
- Ceres seq\_id 1498801

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 661
- Ceres seq\_id 1498802
- Location of start within SEQ ID NO 660: at 179 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6362
- Mitochondrial carrier proteins
- Location within SEQ ID NO 661: from 37 to 321 aa.
- Alignment No. 6363
- Mitochondrial carrier proteins
- Location within SEQ ID NO 661: from 137 to 324 aa.
- Alignment No. 6364
- Mitochondrial carrier proteins
- Location within SEQ ID NO 661: from 232 to 331 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6365
- gi No. 3150404
- % Identity 99.4
- Alignment Length 331
- Location of Alignment in SEQ ID NO 661: from 1 to 331
- Alignment No. 6366
- gi No. 3378495
- % Identity 70.9
- Alignment Length 289
- Location of Alignment in SEQ ID NO 661: from 42 to 330

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 662
- Ceres seq\_id 1498803
- Location of start within SEQ ID NO 660: at 302 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6367
- Mitochondrial carrier proteins
- Location within SEQ ID NO 662: from 1 to 280 aa.
- Alignment No. 6368
- Mitochondrial carrier proteins
- Location within SEQ ID NO 662: from 96 to 283 aa.
- Alignment No. 6369
- Mitochondrial carrier proteins
- Location within SEQ ID NO 662: from 191 to 290 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6370
- gi No. 3150404

- % Identity 99.4
- Alignment Length 331
- Location of Alignment in SEQ ID NO 662: from 1 to 290
- Alignment No. 6371
- gi No. 3378495
- % Identity 70.9
- Alignment Length 289
- Location of Alignment in SEQ ID NO 662: from 1 to 289

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 663
- Ceres seq\_id 1498804
- Location of start within SEQ ID NO 660: at 338 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6372
- Mitochondrial carrier proteins
- Location within SEQ ID NO 663: from 1 to 268 aa.
- Alignment No. 6373
- Mitochondrial carrier proteins
- Location within SEQ ID NO 663: from 84 to 271 aa.
- Alignment No. 6374
- Mitochondrial carrier proteins
- Location within SEQ ID NO 663: from 179 to 278 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6375
- gi No. 3150404
- % Identity 99.4
- Alignment Length 331
- Location of Alignment in SEQ ID NO 663: from 1 to 278
- Alignment No. 6376
- gi No. 3378495
- % Identity 70.9
- Alignment Length 289
- Location of Alignment in SEQ ID NO 663: from 1 to 277

Maximum Length Sequence corresponding to clone ID 150798

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 664
- Ceres seq\_id 1498808

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 665
- Ceres seq\_id 1498809
- Location of start within SEQ ID NO 664: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6377
- Plant lipid transfer protein family
- Location within SEQ ID NO 665: from 211 to 293 aa.
- Alignment No. 6378
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 665: from 39 to 143 aa.

- Alignment No. 6379
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 665: from 47 to 171 aa.
  
- Alignment No. 6380
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 665: from 62 to 203 aa.
  
- Alignment No. 6381
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 665: from 92 to 203 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6382
- gi No. 4662641
- % Identity 98.3
- Alignment Length 291
- Location of Alignment in SEQ ID NO 665: from 7 to 294

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 666
- Ceres seq\_id 1498810
- Location of start within SEQ ID NO 664: at 20 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6383
- Plant lipid transfer protein family
- Location within SEQ ID NO 666: from 205 to 287 aa.
  
- Alignment No. 6384
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 666: from 33 to 137 aa.
  
- Alignment No. 6385
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 666: from 41 to 165 aa.
  
- Alignment No. 6386
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 666: from 56 to 197 aa.
  
- Alignment No. 6387
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 666: from 86 to 197 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6388
- gi No. 4662641
- % Identity 98.3
- Alignment Length 291
- Location of Alignment in SEQ ID NO 666: from 1 to 288

Maximum Length Sequence corresponding to clone ID 150889

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 667
- Ceres seq\_id 1498811

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 668
- Ceres seq\_id 1498812
- Location of start within SEQ ID NO 667: at 773 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6389
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 668: from 16 to 108 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 669
- Ceres seq\_id 1498813
- Location of start within SEQ ID NO 667: at 902 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6390
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 669: from 1 to 65 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 670
- Ceres seq\_id 1498814
- Location of start within SEQ ID NO 667: at 965 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 150983

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 671
- Ceres seq\_id 1498815

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 672
- Ceres seq\_id 1498816
- Location of start within SEQ ID NO 671: at 307 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6391
- gi No. 1944132
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 672: from 1 to 107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 673
- Ceres seq\_id 1498817
- Location of start within SEQ ID NO 671: at 364 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6392
- gi No. 1944132
- % Identity 74.8
- Alignment Length 111

- Location of Alignment in SEQ ID NO 673: from 1 to 88

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 674
- Ceres seq\_id 1498818
- Location of start within SEQ ID NO 671: at 454 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6393
- gi No. 1944132
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 674: from 1 to 58

Maximum Length Sequence corresponding to clone ID 151244

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 675
- Ceres seq\_id 1498823

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 676
- Ceres seq\_id 1498824
- Location of start within SEQ ID NO 675: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6394
- Glycosyl transferases
- Location within SEQ ID NO 676: from 148 to 298 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6395
- gi No. 2245014
- % Identity 100
- Alignment Length 351
- Location of Alignment in SEQ ID NO 676: from 223 to 573
- Alignment No. 6396
- gi No. 4584546
- % Identity 79
- Alignment Length 119
- Location of Alignment in SEQ ID NO 676: from 395 to 513
- Alignment No. 6397
- gi No. 4584546
- % Identity 73.8
- Alignment Length 264
- Location of Alignment in SEQ ID NO 676: from 109 to 371

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 677
- Ceres seq\_id 1498825
- Location of start within SEQ ID NO 675: at 61 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6398
- Glycosyl transferases
- Location within SEQ ID NO 677: from 128 to 278 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6399
- gi No. 2245014
- % Identity 100
- Alignment Length 351
- Location of Alignment in SEQ ID NO 677: from 203 to 553
  
- Alignment No. 6400
- gi No. 4584546
- % Identity 79
- Alignment Length 119
- Location of Alignment in SEQ ID NO 677: from 375 to 493
  
- Alignment No. 6401
- gi No. 4584546
- % Identity 73.8
- Alignment Length 264
- Location of Alignment in SEQ ID NO 677: from 89 to 351

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 678
- Ceres seq\_id 1498826
- Location of start within SEQ ID NO 675: at 280 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6402
- Glycosyl transferases
- Location within SEQ ID NO 678: from 55 to 205 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6403
- gi No. 2245014
- % Identity 100
- Alignment Length 351
- Location of Alignment in SEQ ID NO 678: from 130 to 480
  
- Alignment No. 6404
- gi No. 4584546
- % Identity 79
- Alignment Length 119
- Location of Alignment in SEQ ID NO 678: from 302 to 420
  
- Alignment No. 6405
- gi No. 4584546
- % Identity 73.8
- Alignment Length 264
- Location of Alignment in SEQ ID NO 678: from 16 to 278

Maximum Length Sequence corresponding to clone ID 151489

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 679
- Ceres seq\_id 1498829

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 680
- Ceres seq\_id 1498830
- Location of start within SEQ ID NO 679: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6406
- gi No. 2660664
- % Identity 72.5
- Alignment Length 109
- Location of Alignment in SEQ ID NO 680: from 1 to 108
  
- Alignment No. 6407
- gi No. 2827649
- % Identity 70.6
- Alignment Length 109
- Location of Alignment in SEQ ID NO 680: from 1 to 108
  
- Alignment No. 6408
- gi No. 4512625
- % Identity 100
- Alignment Length 109
- Location of Alignment in SEQ ID NO 680: from 1 to 108

Maximum Length Sequence corresponding to clone ID 151518

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 681
- Ceres seq\_id 1498831

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 682
- Ceres seq\_id 1498832
- Location of start within SEQ ID NO 681: at 145 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6409
- gi No. 2827536
- % Identity 87.7
- Alignment Length 195
- Location of Alignment in SEQ ID NO 682: from 1 to 150

Maximum Length Sequence corresponding to clone ID 152094

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 683
- Ceres seq\_id 1498841

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 684
- Ceres seq\_id 1498842
- Location of start within SEQ ID NO 683: at 82 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6410
- Peroxidase
- Location within SEQ ID NO 684: from 39 to 118 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6411
- gi No. 1546706
- % Identity 90.7
- Alignment Length 118
- Location of Alignment in SEQ ID NO 684: from 1 to 118
  
- Alignment No. 6412
- gi No. 1620369
- % Identity 73.7



- Alignment Length 114
- Location of Alignment in SEQ ID NO 684: from 6 to 118
- Alignment No. 6413
- gi No. 3004558
- % Identity 73.7
- Alignment Length 114
- Location of Alignment in SEQ ID NO 684: from 6 to 118

Maximum Length Sequence corresponding to clone ID 152141

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 685
- Ceres seq\_id 1498843

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 686
- Ceres seq\_id 1498844
- Location of start within SEQ ID NO 685: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6414
- Isocitrate and isopropylmalate dehydrogenases
- Location within SEQ ID NO 686: from 56 to 174 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6415
- gi No. 126201
- % Identity 87.8
- Alignment Length 164
- Location of Alignment in SEQ ID NO 686: from 13 to 174
- Alignment No. 6416
- gi No. 1903021
- % Identity 100
- Alignment Length 163
- Location of Alignment in SEQ ID NO 686: from 13 to 174
- Alignment No. 6417
- gi No. 4512615
- % Identity 74.4
- Alignment Length 164
- Location of Alignment in SEQ ID NO 686: from 13 to 174

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 687
- Ceres seq\_id 1498845
- Location of start within SEQ ID NO 685: at 39 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6418
- Isocitrate and isopropylmalate dehydrogenases
- Location within SEQ ID NO 687: from 44 to 162 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6419
- gi No. 126201
- % Identity 87.8
- Alignment Length 164
- Location of Alignment in SEQ ID NO 687: from 1 to 162

- Alignment No. 6420
- gi No. 1903021
- % Identity 100
- Alignment Length 163
- Location of Alignment in SEQ ID NO 687: from 1 to 162
- Alignment No. 6421
- gi No. 4512615
- % Identity 74.4
- Alignment Length 164
- Location of Alignment in SEQ ID NO 687: from 1 to 162

Maximum Length Sequence corresponding to clone ID 152232

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 688
- Ceres seq\_id 1498846

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 689
- Ceres seq\_id 1498847
- Location of start within SEQ ID NO 688: at 327 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6422
- Uncharacterized protein family UPF0023
- Location within SEQ ID NO 689: from 1 to 167 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 690
- Ceres seq\_id 1498848
- Location of start within SEQ ID NO 688: at 459 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6423
- Uncharacterized protein family UPF0023
- Location within SEQ ID NO 690: from 1 to 123 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 691
- Ceres seq\_id 1498849
- Location of start within SEQ ID NO 688: at 507 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6424
- Uncharacterized protein family UPF0023
- Location within SEQ ID NO 691: from 1 to 107 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 152458

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 692
- Ceres seq\_id 1498854

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 693

- Ceres seq\_id 1498855
- Location of start within SEQ ID NO 692: at 120 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6425
- gi No. 1076618
- % Identity 72.2
- Alignment Length 255
- Location of Alignment in SEQ ID NO 693: from 64 to 318
- Alignment No. 6426
- gi No. 1478343
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 693: from 191 to 230
- Alignment No. 6427
- gi No. 1588565
- % Identity 70.8
- Alignment Length 253
- Location of Alignment in SEQ ID NO 693: from 66 to 318
- Alignment No. 6428
- gi No. 1872517
- % Identity 74.7
- Alignment Length 253
- Location of Alignment in SEQ ID NO 693: from 66 to 318
- Alignment No. 6429
- gi No. 2811176
- % Identity 79.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 693: from 143 to 291
- Alignment No. 6430
- gi No. 3023316
- % Identity 71.4
- Alignment Length 255
- Location of Alignment in SEQ ID NO 693: from 64 to 318
- Alignment No. 6431
- gi No. 3218543
- % Identity 71.5
- Alignment Length 253
- Location of Alignment in SEQ ID NO 693: from 66 to 318
- Alignment No. 6432
- gi No. 322692
- % Identity 71.9
- Alignment Length 253
- Location of Alignment in SEQ ID NO 693: from 66 to 318
- Alignment No. 6433
- gi No. 3334449
- % Identity 71.9
- Alignment Length 253
- Location of Alignment in SEQ ID NO 693: from 66 to 318
- Alignment No. 6434

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- gi No. 3599419
- % Identity 71.1
- Alignment Length 253
- Location of Alignment in SEQ ID NO 693: from 66 to 318
  
- Alignment No. 6435
- gi No. 3913066
- % Identity 72.5
- Alignment Length 255
- Location of Alignment in SEQ ID NO 693: from 64 to 318
  
- Alignment No. 6436
- gi No. 3913143
- % Identity 72.3
- Alignment Length 253
- Location of Alignment in SEQ ID NO 693: from 66 to 318
  
- Alignment No. 6437
- gi No. 3915618
- % Identity 71
- Alignment Length 252
- Location of Alignment in SEQ ID NO 693: from 67 to 318
  
- Alignment No. 6438
- gi No. 3915639
- % Identity 74.7
- Alignment Length 253
- Location of Alignment in SEQ ID NO 693: from 66 to 318
  
- Alignment No. 6439
- gi No. 421824
- % Identity 74.7
- Alignment Length 253
- Location of Alignment in SEQ ID NO 693: from 66 to 318
  
- Alignment No. 6440
- gi No. 631919
- % Identity 71
- Alignment Length 252
- Location of Alignment in SEQ ID NO 693: from 67 to 318

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 694
- Ceres seq\_id 1498856
- Location of start within SEQ ID NO 692: at 537 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6441
- gi No. 1076618
- % Identity 72.2
- Alignment Length 255
- Location of Alignment in SEQ ID NO 694: from 1 to 179
  
- Alignment No. 6442
- gi No. 1478343
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 694: from 52 to 91

- Alignment No. 6443
- gi No. 1588565
- % Identity 70.8
- Alignment Length 253
- Location of Alignment in SEQ ID NO 694: from 1 to 179
  
- Alignment No. 6444
- gi No. 1872517
- % Identity 74.7
- Alignment Length 253
- Location of Alignment in SEQ ID NO 694: from 1 to 179
  
- Alignment No. 6445
- gi No. 2811176
- % Identity 79.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 694: from 4 to 152
  
- Alignment No. 6446
- gi No. 3023316
- % Identity 71.4
- Alignment Length 255
- Location of Alignment in SEQ ID NO 694: from 1 to 179
  
- Alignment No. 6447
- gi No. 3218543
- % Identity 71.5
- Alignment Length 253
- Location of Alignment in SEQ ID NO 694: from 1 to 179
  
- Alignment No. 6448
- gi No. 322692
- % Identity 71.9
- Alignment Length 253
- Location of Alignment in SEQ ID NO 694: from 1 to 179
  
- Alignment No. 6449
- gi No. 3334449
- % Identity 71.9
- Alignment Length 253
- Location of Alignment in SEQ ID NO 694: from 1 to 179
  
- Alignment No. 6450
- gi No. 3599419
- % Identity 71.1
- Alignment Length 253
- Location of Alignment in SEQ ID NO 694: from 1 to 179
  
- Alignment No. 6451
- gi No. 3913066
- % Identity 72.5
- Alignment Length 255
- Location of Alignment in SEQ ID NO 694: from 1 to 179
  
- Alignment No. 6452
- gi No. 3913143
- % Identity 72.3
- Alignment Length 253
- Location of Alignment in SEQ ID NO 694: from 1 to 179
  
- Alignment No. 6453

- gi No. 3915618
- % Identity 71
- Alignment Length 252
- Location of Alignment in SEQ ID NO 694: from 1 to 179
  
- Alignment No. 6454
- gi No. 3915639
- % Identity 74.7
- Alignment Length 253
- Location of Alignment in SEQ ID NO 694: from 1 to 179
  
- Alignment No. 6455
- gi No. 421824
- % Identity 74.7
- Alignment Length 253
- Location of Alignment in SEQ ID NO 694: from 1 to 179
  
- Alignment No. 6456
- gi No. 631919
- % Identity 71
- Alignment Length 252
- Location of Alignment in SEQ ID NO 694: from 1 to 179

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 695
- Ceres seq\_id 1498857
- Location of start within SEQ ID NO 692: at 549 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6457
- gi No. 1076618
- % Identity 72.2
- Alignment Length 255
- Location of Alignment in SEQ ID NO 695: from 1 to 175
  
- Alignment No. 6458
- gi No. 1478343
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 695: from 48 to 87
  
- Alignment No. 6459
- gi No. 1588565
- % Identity 70.8
- Alignment Length 253
- Location of Alignment in SEQ ID NO 695: from 1 to 175
  
- Alignment No. 6460
- gi No. 1872517
- % Identity 74.7
- Alignment Length 253
- Location of Alignment in SEQ ID NO 695: from 1 to 175
  
- Alignment No. 6461
- gi No. 2811176
- % Identity 79.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 695: from 1 to 148

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- [illegible]

- gi No. 631919
- % Identity 71
- Alignment Length 252
- Location of Alignment in SEQ ID NO 695: from 1 to 175

Maximum Length Sequence corresponding to clone ID 152627

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 696
- Ceres seq\_id 1498858

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 697
- Ceres seq\_id 1498859
- Location of start within SEQ ID NO 696: at 63 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6473
- tRNA synthetases class II (A)
- Location within SEQ ID NO 697: from 27 to 253 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 698
- Ceres seq\_id 1498860
- Location of start within SEQ ID NO 696: at 102 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6474
- tRNA synthetases class II (A)
- Location within SEQ ID NO 698: from 14 to 240 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 699
- Ceres seq\_id 1498861
- Location of start within SEQ ID NO 696: at 435 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6475
- tRNA synthetases class II (A)
- Location within SEQ ID NO 699: from 1 to 129 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 153160

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 700
- Ceres seq\_id 1498874

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 701
- Ceres seq\_id 1498875
- Location of start within SEQ ID NO 700: at 493 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6476
- DedA family



- Location within SEQ ID NO 701: from 24 to 144 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6477
- gi No. 2245138
- % Identity 76.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 701: from 10 to 146

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 702
- Ceres seq\_id 1498876
- Location of start within SEQ ID NO 700: at 499 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6478
- DedA family
- Location within SEQ ID NO 702: from 22 to 142 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6479
- gi No. 2245138
- % Identity 76.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 702: from 8 to 144

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 703
- Ceres seq\_id 1498877
- Location of start within SEQ ID NO 700: at 550 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6480
- DedA family
- Location within SEQ ID NO 703: from 5 to 125 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6481
- gi No. 2245138
- % Identity 76.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 703: from 1 to 127

Maximum Length Sequence corresponding to clone ID 153249

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 704
- Ceres seq\_id 1498878

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 705
- Ceres seq\_id 1498879
- Location of start within SEQ ID NO 704: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6482
- gi No. 2435521
- % Identity 95.7
- Alignment Length 463

- Location of Alignment in SEQ ID NO 705: from 11 to 473

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 706
- Ceres seq\_id 1498880
- Location of start within SEQ ID NO 704: at 32 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6483
- gi No. 2435521
- % Identity 95.7
- Alignment Length 463
- Location of Alignment in SEQ ID NO 706: from 1 to 463

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 707
- Ceres seq\_id 1498881
- Location of start within SEQ ID NO 704: at 365 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6484
- gi No. 2435521
- % Identity 95.7
- Alignment Length 463
- Location of Alignment in SEQ ID NO 707: from 1 to 352

Maximum Length Sequence corresponding to clone ID 153259

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 708
- Ceres seq\_id 1498882

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 709
- Ceres seq\_id 1498883
- Location of start within SEQ ID NO 708: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 710
- Ceres seq\_id 1498884
- Location of start within SEQ ID NO 708: at 315 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6485
- gi No. 2245009
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 710: from 22 to 40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 711
- Ceres seq\_id 1498885
- Location of start within SEQ ID NO 708: at 520 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6486
- gi No. 2245009
- % Identity 91.5
- Alignment Length 71
- Location of Alignment in SEQ ID NO 711: from 1 to 37
  
- Alignment No. 6487
- gi No. 3461825
- % Identity 100
- Alignment Length 67
- Location of Alignment in SEQ ID NO 711: from 1 to 37

Maximum Length Sequence corresponding to clone ID 153418

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 712
- Ceres seq\_id 1498886

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 713
- Ceres seq\_id 1498887
- Location of start within SEQ ID NO 712: at 43 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6488
- UDP-glucuronosyl and UDP-glucosyl transferases
- Location within SEQ ID NO 713: from 319 to 389 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6489
- gi No. 3757518
- % Identity 99.2
- Alignment Length 478
- Location of Alignment in SEQ ID NO 713: from 1 to 478

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 714
- Ceres seq\_id 1498888
- Location of start within SEQ ID NO 712: at 88 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6490
- UDP-glucuronosyl and UDP-glucosyl transferases
- Location within SEQ ID NO 714: from 304 to 374 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6491
- gi No. 3757518
- % Identity 99.2
- Alignment Length 478
- Location of Alignment in SEQ ID NO 714: from 1 to 463

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 715
- Ceres seq\_id 1498889
- Location of start within SEQ ID NO 712: at 316 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6492
- UDP-glucuronosyl and UDP-glucosyl transferases
- Location within SEQ ID NO 715: from 228 to 298 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6493
- gi No. 3757518
- % Identity 99.2
- Alignment Length 478
- Location of Alignment in SEQ ID NO 715: from 1 to 387

Maximum Length Sequence corresponding to clone ID 153541

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 716
- Ceres seq\_id 1498890

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 717
- Ceres seq\_id 1498891
- Location of start within SEQ ID NO 716: at 412 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6494
- Fatty acid desaturase
- Location within SEQ ID NO 717: from 1 to 328 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6495
- gi No. 100145
- % Identity 86.5
- Alignment Length 355
- Location of Alignment in SEQ ID NO 717: from 1 to 332
- Alignment No. 6496
- gi No. 1020096
- % Identity 86.4
- Alignment Length 361
- Location of Alignment in SEQ ID NO 717: from 1 to 332
- Alignment No. 6497
- gi No. 1174466
- % Identity 79.7
- Alignment Length 354
- Location of Alignment in SEQ ID NO 717: from 1 to 332
- Alignment No. 6498
- gi No. 134943
- % Identity 95.5
- Alignment Length 355
- Location of Alignment in SEQ ID NO 717: from 1 to 332
- Alignment No. 6499
- gi No. 134944
- % Identity 85.3
- Alignment Length 354
- Location of Alignment in SEQ ID NO 717: from 1 to 332
- Alignment No. 6500
- gi No. 134945

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- % Identity 88.9
- Alignment Length 361
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6501
- gi No. 134946
- % Identity 83.1
- Alignment Length 355
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6502
- gi No. 1785862
- % Identity 82.8
- Alignment Length 354
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6503
- gi No. 2129532
- % Identity 98
- Alignment Length 343
- Location of Alignment in SEQ ID NO 717: from 1 to 319
  
- Alignment No. 6504
- gi No. 2194093
- % Identity 90.1
- Alignment Length 344
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6505
- gi No. 2281099
- % Identity 99.7
- Alignment Length 355
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6506
- gi No. 2290400
- % Identity 87
- Alignment Length 354
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6507
- gi No. 2290402
- % Identity 87.9
- Alignment Length 354
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6508
- gi No. 267036
- % Identity 80
- Alignment Length 355
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6509
- gi No. 267037
- % Identity 94.4
- Alignment Length 355
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6510
- gi No. 2944444
- % Identity 84.2

- Alignment Length 361
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6511
- gi No. 3133287
- % Identity 83
- Alignment Length 223
- Location of Alignment in SEQ ID NO 717: from 110 to 332
  
- Alignment No. 6512
- gi No. 3355632
- % Identity 83.7
- Alignment Length 356
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6513
- gi No. 3355634
- % Identity 83.1
- Alignment Length 356
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6514
- gi No. 3915024
- % Identity 82.8
- Alignment Length 354
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6515
- gi No. 3915029
- % Identity 82.4
- Alignment Length 353
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6516
- gi No. 3915030
- % Identity 83.5
- Alignment Length 351
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6517
- gi No. 3915031
- % Identity 79.2
- Alignment Length 356
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6518
- gi No. 3915032
- % Identity 87.4
- Alignment Length 358
- Location of Alignment in SEQ ID NO 717: from 1 to 329
  
- Alignment No. 6519
- gi No. 3915033
- % Identity 83.3
- Alignment Length 354
- Location of Alignment in SEQ ID NO 717: from 1 to 332
  
- Alignment No. 6520
- gi No. 3915035
- % Identity 85.9
- Alignment Length 354

- Location of Alignment in SEQ ID NO 717: from 1 to 332
- Alignment No. 6521
- gi No. 417820
- % Identity 86.5
- Alignment Length 355
- Location of Alignment in SEQ ID NO 717: from 1 to 332
- Alignment No. 6522
- gi No. 417821
- % Identity 78.1
- Alignment Length 357
- Location of Alignment in SEQ ID NO 717: from 1 to 332
- Alignment No. 6523
- gi No. 4929208
- % Identity 90.7
- Alignment Length 150
- Location of Alignment in SEQ ID NO 717: from 110 to 259
- Alignment No. 6524
- gi No. 5114269
- % Identity 94.4
- Alignment Length 355
- Location of Alignment in SEQ ID NO 717: from 1 to 332
- Alignment No. 6525
- gi No. 512398
- % Identity 94.6
- Alignment Length 355
- Location of Alignment in SEQ ID NO 717: from 1 to 332
- Alignment No. 6526
- gi No. 533082
- % Identity 84.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 717: from 1 to 332
- Alignment No. 6527
- gi No. 533084
- % Identity 81.7
- Alignment Length 349
- Location of Alignment in SEQ ID NO 717: from 1 to 332
- Alignment No. 6528
- gi No. 533086
- % Identity 78.2
- Alignment Length 354
- Location of Alignment in SEQ ID NO 717: from 1 to 332
- Alignment No. 6529
- gi No. 5726639
- % Identity 85.2
- Alignment Length 358
- Location of Alignment in SEQ ID NO 717: from 1 to 332
- Alignment No. 6530
- gi No. 575942
- % Identity 87
- Alignment Length 361
- Location of Alignment in SEQ ID NO 717: from 1 to 332

- Alignment No. 6531
- gi No. 736721
- % Identity 82.6
- Alignment Length 167
- Location of Alignment in SEQ ID NO 717: from 166 to 332
  
- Alignment No. 6532
- gi No. 951427
- % Identity 88.9
- Alignment Length 361
- Location of Alignment in SEQ ID NO 717: from 1 to 332

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 718
- Ceres seq\_id 1498892
- Location of start within SEQ ID NO 716: at 445 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6533
- Fatty acid desaturase
- Location within SEQ ID NO 718: from 1 to 317 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6534
- gi No. 100145
- % Identity 86.5
- Alignment Length 355
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6535
- gi No. 1020096
- % Identity 86.4
- Alignment Length 361
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6536
- gi No. 1174466
- % Identity 79.7
- Alignment Length 354
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6537
- gi No. 134943
- % Identity 95.5
- Alignment Length 355
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6538
- gi No. 134944
- % Identity 85.3
- Alignment Length 354
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6539
- gi No. 134945
- % Identity 88.9
- Alignment Length 361
- Location of Alignment in SEQ ID NO 718: from 1 to 321



- Alignment No. 6540
- gi No. 134946
- % Identity 83.1
- Alignment Length 355
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6541
- gi No. 1785862
- % Identity 82.8
- Alignment Length 354
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6542
- gi No. 2129532
- % Identity 98
- Alignment Length 343
- Location of Alignment in SEQ ID NO 718: from 1 to 308
  
- Alignment No. 6543
- gi No. 2194093
- % Identity 90.1
- Alignment Length 344
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6544
- gi No. 2281099
- % Identity 99.7
- Alignment Length 355
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6545
- gi No. 2290400
- % Identity 87
- Alignment Length 354
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6546
- gi No. 2290402
- % Identity 87.9
- Alignment Length 354
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6547
- gi No. 267036
- % Identity 80
- Alignment Length 355
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6548
- gi No. 267037
- % Identity 94.4
- Alignment Length 355
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6549
- gi No. 2944444
- % Identity 84.2
- Alignment Length 361
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6550

- gi No. 3133287
- % Identity 83
- Alignment Length 223
- Location of Alignment in SEQ ID NO 718: from 99 to 321
  
- Alignment No. 6551
- gi No. 3355632
- % Identity 83.7
- Alignment Length 356
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6552
- gi No. 3355634
- % Identity 83.1
- Alignment Length 356
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6553
- gi No. 3915024
- % Identity 82.8
- Alignment Length 354
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6554
- gi No. 3915029
- % Identity 82.4
- Alignment Length 353
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6555
- gi No. 3915030
- % Identity 83.5
- Alignment Length 351
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6556
- gi No. 3915031
- % Identity 79.2
- Alignment Length 356
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6557
- gi No. 3915032
- % Identity 87.4
- Alignment Length 358
- Location of Alignment in SEQ ID NO 718: from 1 to 318
  
- Alignment No. 6558
- gi No. 3915033
- % Identity 83.3
- Alignment Length 354
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6559
- gi No. 3915035
- % Identity 85.9
- Alignment Length 354
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6560
- gi No. 417820

- % Identity 86.5
- Alignment Length 355
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6561
- gi No. 417821
- % Identity 78.1
- Alignment Length 357
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6562
- gi No. 4929208
- % Identity 90.7
- Alignment Length 150
- Location of Alignment in SEQ ID NO 718: from 99 to 248
  
- Alignment No. 6563
- gi No. 5114269
- % Identity 94.4
- Alignment Length 355
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6564
- gi No. 512398
- % Identity 94.6
- Alignment Length 355
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6565
- gi No. 533082
- % Identity 84.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6566
- gi No. 533084
- % Identity 81.7
- Alignment Length 349
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6567
- gi No. 533086
- % Identity 78.2
- Alignment Length 354
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6568
- gi No. 5726639
- % Identity 85.2
- Alignment Length 358
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6569
- gi No. 575942
- % Identity 87
- Alignment Length 361
- Location of Alignment in SEQ ID NO 718: from 1 to 321
  
- Alignment No. 6570
- gi No. 736721
- % Identity 82.6

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- Alignment Length 167
- Location of Alignment in SEQ ID NO 718: from 155 to 321

- Alignment No. 6571
- gi No. 951427
- % Identity 88.9
- Alignment Length 361
- Location of Alignment in SEQ ID NO 718: from 1 to 321
```

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 719
- Ceres seq_id 1498893
- Location of start within SEQ ID NO 716: at 622 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6572
- Fatty acid desaturase
- Location within SEQ ID NO 719: from 1 to 258 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6573
 - gi No. 100145
 - % Identity 86.5
 - Alignment Length 355
 - Location of Alignment in SEQ ID NO 719: from 1 to 262
- Alignment No. 6574
 - gi No. 1020096
 - % Identity 86.4
 - Alignment Length 361
 - Location of Alignment in SEQ ID NO 719: from 1 to 262
- Alignment No. 6575
 - gi No. 1174466
 - % Identity 79.7
 - Alignment Length 354
 - Location of Alignment in SEQ ID NO 719: from 1 to 262
- Alignment No. 6576
 - gi No. 134943
 - % Identity 95.5
 - Alignment Length 355
 - Location of Alignment in SEQ ID NO 719: from 1 to 262
- Alignment No. 6577
 - gi No. 134944
 - % Identity 85.3
 - Alignment Length 354
 - Location of Alignment in SEQ ID NO 719: from 1 to 262
- Alignment No. 6578
 - gi No. 134945
 - % Identity 88.9
 - Alignment Length 361
 - Location of Alignment in SEQ ID NO 719: from 1 to 262
- Alignment No. 6579
 - gi No. 134946
 - % Identity 83.1
 - Alignment Length 355

- Location of Alignment in SEQ ID NO 719: from 1 to 262
- Alignment No. 6580
- gi No. 1785862
- % Identity 82.8
- Alignment Length 354
- Location of Alignment in SEQ ID NO 719: from 1 to 262
- Alignment No. 6581
- gi No. 2129532
- % Identity 98
- Alignment Length 343
- Location of Alignment in SEQ ID NO 719: from 1 to 249
- Alignment No. 6582
- gi No. 2194093
- % Identity 90.1
- Alignment Length 344
- Location of Alignment in SEQ ID NO 719: from 1 to 262
- Alignment No. 6583
- gi No. 2281099
- % Identity 99.7
- Alignment Length 355
- Location of Alignment in SEQ ID NO 719: from 1 to 262
- Alignment No. 6584
- gi No. 2290400
- % Identity 87
- Alignment Length 354
- Location of Alignment in SEQ ID NO 719: from 1 to 262
- Alignment No. 6585
- gi No. 2290402
- % Identity 87.9
- Alignment Length 354
- Location of Alignment in SEQ ID NO 719: from 1 to 262
- Alignment No. 6586
- gi No. 267036
- % Identity 80
- Alignment Length 355
- Location of Alignment in SEQ ID NO 719: from 1 to 262
- Alignment No. 6587
- gi No. 267037
- % Identity 94.4
- Alignment Length 355
- Location of Alignment in SEQ ID NO 719: from 1 to 262
- Alignment No. 6588
- gi No. 2944444
- % Identity 84.2
- Alignment Length 361
- Location of Alignment in SEQ ID NO 719: from 1 to 262
- Alignment No. 6589
- gi No. 3133287
- % Identity 83
- Alignment Length 223
- Location of Alignment in SEQ ID NO 719: from 40 to 262

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- Alignment No. 6590
- gi No. 3355632
- % Identity 83.7
- Alignment Length 356
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6591
- gi No. 3355634
- % Identity 83.1
- Alignment Length 356
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6592
- gi No. 3915024
- % Identity 82.8
- Alignment Length 354
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6593
- gi No. 3915029
- % Identity 82.4
- Alignment Length 353
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6594
- gi No. 3915030
- % Identity 83.5
- Alignment Length 351
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6595
- gi No. 3915031
- % Identity 79.2
- Alignment Length 356
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6596
- gi No. 3915032
- % Identity 87.4
- Alignment Length 358
- Location of Alignment in SEQ ID NO 719: from 1 to 259

- Alignment No. 6597
- gi No. 3915033
- % Identity 83.3
- Alignment Length 354
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6598
- gi No. 3915035
- % Identity 85.9
- Alignment Length 354
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6599
- gi No. 417820
- % Identity 86.5
- Alignment Length 355
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6600
- gi No. 417821
- % Identity 78.1
- Alignment Length 357
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6601
- gi No. 4929208
- % Identity 90.7
- Alignment Length 150
- Location of Alignment in SEQ ID NO 719: from 40 to 189

- Alignment No. 6602
- gi No. 5114269
- % Identity 94.4
- Alignment Length 355
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6603
- gi No. 512398
- % Identity 94.6
- Alignment Length 355
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6604
- gi No. 533082
- % Identity 84.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6605
- gi No. 533084
- % Identity 81.7
- Alignment Length 349
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6606
- gi No. 533086
- % Identity 78.2
- Alignment Length 354
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6607
- gi No. 5726639
- % Identity 85.2
- Alignment Length 358
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6608
- gi No. 575942
- % Identity 87
- Alignment Length 361
- Location of Alignment in SEQ ID NO 719: from 1 to 262

- Alignment No. 6609
- gi No. 736721
- % Identity 82.6
- Alignment Length 167
- Location of Alignment in SEQ ID NO 719: from 96 to 262

- Alignment No. 6610

- gi No. 951427
- % Identity 88.9
- Alignment Length 361
- Location of Alignment in SEQ ID NO 719: from 1 to 262

Maximum Length Sequence corresponding to clone ID 153846

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 720
- Ceres seq_id 1498905

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 721
- Ceres seq_id 1498906
- Location of start within SEQ ID NO 720: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6611
- Uncharacterized protein family UPF0015
- Location within SEQ ID NO 721: from 60 to 290 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 722
- Ceres seq_id 1498907
- Location of start within SEQ ID NO 720: at 59 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6612
- Uncharacterized protein family UPF0015
- Location within SEQ ID NO 722: from 41 to 271 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 723
- Ceres seq_id 1498908
- Location of start within SEQ ID NO 720: at 110 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6613
- Uncharacterized protein family UPF0015
- Location within SEQ ID NO 723: from 24 to 254 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 154037

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 724
- Ceres seq_id 1498912

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 725
- Ceres seq_id 1498913
- Location of start within SEQ ID NO 724: at 30 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6614
- S-locus glycoprotein family

- Location within SEQ ID NO 725: from 19 to 208 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 726
- Ceres seq_id 1498914
- Location of start within SEQ ID NO 724: at 809 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 154343

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 727
- Ceres seq_id 1498918

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 728
- Ceres seq_id 1498919
- Location of start within SEQ ID NO 727: at 137 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6615
- Myb-like DNA-binding domain
- Location within SEQ ID NO 728: from 14 to 61 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6616
- gi No. 1044916
- % Identity 76.2
- Alignment Length 63
- Location of Alignment in SEQ ID NO 728: from 1 to 63
- Alignment No. 6617
- gi No. 1945283
- % Identity 70.1
- Alignment Length 168
- Location of Alignment in SEQ ID NO 728: from 1 to 167
- Alignment No. 6618
- gi No. 1946267
- % Identity 71.9
- Alignment Length 128
- Location of Alignment in SEQ ID NO 728: from 1 to 128
- Alignment No. 6619
- gi No. 2129563
- % Identity 71.1
- Alignment Length 128
- Location of Alignment in SEQ ID NO 728: from 1 to 128
- Alignment No. 6620
- gi No. 2129592
- % Identity 70
- Alignment Length 130
- Location of Alignment in SEQ ID NO 728: from 1 to 128
- Alignment No. 6621
- gi No. 2130046

- % Identity 70.1
- Alignment Length 117
- Location of Alignment in SEQ ID NO 728: from 1 to 117

- Alignment No. 6622
- gi No. 2827545
- % Identity 98.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 728: from 201 to 266

- Alignment No. 6623
- gi No. 2827545
- % Identity 96.7
- Alignment Length 92
- Location of Alignment in SEQ ID NO 728: from 1 to 90

- Alignment No. 6624
- gi No. 282964
- % Identity 70.8
- Alignment Length 130
- Location of Alignment in SEQ ID NO 728: from 1 to 130

- Alignment No. 6625
- gi No. 2832383
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 728: from 55 to 99

- Alignment No. 6626
- gi No. 2832389
- % Identity 82.2
- Alignment Length 45
- Location of Alignment in SEQ ID NO 728: from 55 to 99

- Alignment No. 6627
- gi No. 2832488
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 728: from 55 to 99

- Alignment No. 6628
- gi No. 2832490
- % Identity 77.8
- Alignment Length 45
- Location of Alignment in SEQ ID NO 728: from 55 to 99

- Alignment No. 6629
- gi No. 2832520
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 728: from 55 to 99

- Alignment No. 6630
- gi No. 2832524
- % Identity 73.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 728: from 55 to 99

- Alignment No. 6631
- gi No. 2832528
- % Identity 71.1

- Alignment Length 45
- Location of Alignment in SEQ ID NO 728: from 55 to 99

- Alignment No. 6632
- gi No. 2832530
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 728: from 55 to 99

- Alignment No. 6633
- gi No. 2832546
- % Identity 75.6
- Alignment Length 45
- Location of Alignment in SEQ ID NO 728: from 55 to 99

- Alignment No. 6634
- gi No. 2832568
- % Identity 73.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 728: from 55 to 99

- Alignment No. 6635
- gi No. 3080388
- % Identity 70
- Alignment Length 130
- Location of Alignment in SEQ ID NO 728: from 1 to 128

- Alignment No. 6636
- gi No. 3941414
- % Identity 74.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 728: from 75 to 128

- Alignment No. 6637
- gi No. 3941470
- % Identity 74.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 728: from 75 to 128

- Alignment No. 6638
- gi No. 3941506
- % Identity 70.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 728: from 65 to 128

- Alignment No. 6639
- gi No. 3941526
- % Identity 78.6
- Alignment Length 42
- Location of Alignment in SEQ ID NO 728: from 87 to 128

- Alignment No. 6640
- gi No. 4115565
- % Identity 76.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 728: from 37 to 128

- Alignment No. 6641
- gi No. 5263133
- % Identity 70.7
- Alignment Length 41

- Location of Alignment in SEQ ID NO 728: from 59 to 99
- Alignment No. 6642
- gi No. 5263149
- % Identity 70.7
- Alignment Length 41
- Location of Alignment in SEQ ID NO 728: from 59 to 99
- Alignment No. 6643
- gi No. 5668784
- % Identity 72.7
- Alignment Length 128
- Location of Alignment in SEQ ID NO 728: from 1 to 128
- Alignment No. 6644
- gi No. 629736
- % Identity 70.3
- Alignment Length 128
- Location of Alignment in SEQ ID NO 728: from 1 to 128

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 729
- Ceres seq_id 1498920
- Location of start within SEQ ID NO 727: at 491 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6645
- gi No. 1945283
- % Identity 70.1
- Alignment Length 168
- Location of Alignment in SEQ ID NO 729: from 1 to 49
- Alignment No. 6646
- gi No. 2827545
- % Identity 98.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 729: from 83 to 148
- Alignment No. 6647
- gi No. 282964
- % Identity 70.8
- Alignment Length 130
- Location of Alignment in SEQ ID NO 729: from 1 to 12

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 730
- Ceres seq_id 1498921
- Location of start within SEQ ID NO 727: at 506 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6648
- gi No. 1945283
- % Identity 70.1
- Alignment Length 168
- Location of Alignment in SEQ ID NO 730: from 1 to 44
- Alignment No. 6649

- ```
- gi No. 2827545
- % Identity 98.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 730: from 78 to 143
```

Maximum Length Sequence corresponding to clone ID 154344

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 731  
- Ceres seq\_id 1498922

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 732
- Ceres seq\_id 1498923
- Location of start within SEQ ID NO 731: at 281 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- ```
- Alignment No. 6650
- gi No. 5103821
- % Identity 100
- Alignment Length 159
- Location of Alignment in SEQ ID NO 732: from 1 to 159
```

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 733
- Ceres seq_id 1498924
- Location of start within SEQ ID NO 731: at 317 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

#### (D) Related Amino Acid Sequences

- ```
- Alignment No. 6651
- gi No. 5103821
- % Identity 100
- Alignment Length 159
- Location of Alignment in SEQ ID NO 733: from 1 to 147
```

Maximum Length Sequence corresponding to clone ID 154469

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 734
- Ceres seq id 1498925

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 735
- Ceres seq_id 1498926
- Location of start within SEQ ID NO 734: at 1 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6652
- Glycosyl hydrolases family 17
- Location within SEQ ID NO 735: from 79 to 400 aa.

#### (D) Related Amino Acid Sequences

- ```
- Alignment No. 6653
- gi No. 4220485
- % Identity 100
- Alignment Length 438
- Location of Alignment in SEQ ID NO 735: from 57 to 494
```

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 736

- Ceres seq_id 1498927
- Location of start within SEQ ID NO 734: at 169 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6654
- Glycosyl hydrolases family 17
- Location within SEQ ID NO 736: from 23 to 344 aa.

(D) Related Amino Acid Sequences

- ```
- Alignment No. 6655
- gi No. 4220485
- % Identity 100
- Alignment Length 438
- Location of Alignment in SEQ ID NO 736: from 1 to 438
```

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 737
- Ceres seq_id 1498928
- Location of start within SEQ ID NO 734: at 268 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6656
- Glycosyl hydrolases family 17
- Location within SEQ ID NO 737: from 1 to 311 aa.

(D) Related Amino Acid Sequences

- ```
- Alignment No. 6657
- gi No. 4220485
- % Identity 100
- Alignment Length 438
- Location of Alignment in SEQ ID NO 737: from 1 to 405
```

Maximum Length Sequence corresponding to clone ID 154690

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 738  
- Ceres seq id 1498929

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 739
- Ceres seq_id 1498930
- Location of start within SEQ ID NO 738: at 1 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6658
- Pyridoxal-phosphate dependent enzymes
- Location within SEQ ID NO 739: from 2 to 209 aa.

(D) Related Amino Acid Sequences

- ```
- Alignment No. 6659
- gi No. 2245144
- % Identity 83.9
- Alignment Length 223
- Location of Alignment in SEQ ID NO 739: from 2 to 223

- Alignment No. 6660
- gi No. 4996618
- % Identity 98.7
- Alignment Length 223
- Location of Alignment in SEQ ID NO 739: from 2 to 223
```

- Alignment No. 6661
- gi No. 4996620
- % Identity 71.3
- Alignment Length 223
- Location of Alignment in SEQ ID NO 739: from 2 to 223

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 740
- Ceres seq\_id 1498931
- Location of start within SEQ ID NO 738: at 22 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6662
- Pyridoxal-phosphate dependent enzymes
- Location within SEQ ID NO 740: from 1 to 202 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6663
- gi No. 2245144
- % Identity 83.9
- Alignment Length 223
- Location of Alignment in SEQ ID NO 740: from 1 to 216
  
- Alignment No. 6664
- gi No. 4996618
- % Identity 98.7
- Alignment Length 223
- Location of Alignment in SEQ ID NO 740: from 1 to 216
  
- Alignment No. 6665
- gi No. 4996620
- % Identity 71.3
- Alignment Length 223
- Location of Alignment in SEQ ID NO 740: from 1 to 216

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 741
- Ceres seq\_id 1498932
- Location of start within SEQ ID NO 738: at 34 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6666
- Pyridoxal-phosphate dependent enzymes
- Location within SEQ ID NO 741: from 1 to 198 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6667
- gi No. 2245144
- % Identity 83.9
- Alignment Length 223
- Location of Alignment in SEQ ID NO 741: from 1 to 212
  
- Alignment No. 6668
- gi No. 4996618
- % Identity 98.7
- Alignment Length 223
- Location of Alignment in SEQ ID NO 741: from 1 to 212

- Alignment No. 6669
- gi No. 4996620
- % Identity 71.3
- Alignment Length 223
- Location of Alignment in SEQ ID NO 741: from 1 to 212

Maximum Length Sequence corresponding to clone ID 154698

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 742
- Ceres seq\_id 1498933

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 743
- Ceres seq\_id 1498934
- Location of start within SEQ ID NO 742: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6670
- gi No. 3258571
- % Identity 90.9
- Alignment Length 187
- Location of Alignment in SEQ ID NO 743: from 22 to 130

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 744
- Ceres seq\_id 1498935
- Location of start within SEQ ID NO 742: at 569 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 745
- Ceres seq\_id 1498936
- Location of start within SEQ ID NO 742: at 731 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 154888

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 746
- Ceres seq\_id 1498937

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 747
- Ceres seq\_id 1498938
- Location of start within SEQ ID NO 746: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6671
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 747: from 52 to 204 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6672
- gi No. 3242717
- % Identity 100



- Alignment Length 204
- Location of Alignment in SEQ ID NO 747: from 5 to 208

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 748
- Ceres seq\_id 1498939
- Location of start within SEQ ID NO 746: at 15 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6673
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 748: from 48 to 200 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6674
- gi No. 3242717
- % Identity 100
- Alignment Length 204
- Location of Alignment in SEQ ID NO 748: from 1 to 204

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 749
- Ceres seq\_id 1498940
- Location of start within SEQ ID NO 746: at 231 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6675
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 749: from 1 to 128 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6676
- gi No. 3242717
- % Identity 100
- Alignment Length 204
- Location of Alignment in SEQ ID NO 749: from 1 to 132

Maximum Length Sequence corresponding to clone ID 154983

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 750
- Ceres seq\_id 1498941

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 751
- Ceres seq\_id 1498942
- Location of start within SEQ ID NO 750: at 688 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6677
- Fucosyl transferase
- Location within SEQ ID NO 751: from 11 to 217 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6678
- gi No. 5702039
- % Identity 74.5
- Alignment Length 329
- Location of Alignment in SEQ ID NO 751: from 10 to 338

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 752
  - Ceres seq\_id 1498943
  - Location of start within SEQ ID NO 750: at 733 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6679
- Fucosyl transferase
- Location within SEQ ID NO 752: from 1 to 202 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6680
- gi No. 5702039
- % Identity 74.5
- Alignment Length 329
- Location of Alignment in SEQ ID NO 752: from 1 to 323

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 753
- Ceres seq\_id 1498944
- Location of start within SEQ ID NO 750: at 796 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6681
- Fucosyl transferase
- Location within SEQ ID NO 753: from 1 to 181 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6682
- gi No. 5702039
- % Identity 74.5
- Alignment Length 329
- Location of Alignment in SEQ ID NO 753: from 1 to 302

Maximum Length Sequence corresponding to clone ID 155143

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 754
- Ceres seq\_id 1498949

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 755
- Ceres seq\_id 1498950
- Location of start within SEQ ID NO 754: at 32 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6683
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 755: from 90 to 383 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6684
- gi No. 2465008
- % Identity 70.5
- Alignment Length 315
- Location of Alignment in SEQ ID NO 755: from 73 to 386
- Alignment No. 6685
- gi No. 4056456
- % Identity 98.4

- Alignment Length 309
- Location of Alignment in SEQ ID NO 755: from 78 to 386

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 756
- Ceres seq\_id 1498951
- Location of start within SEQ ID NO 754: at 263 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6686
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 756: from 13 to 306 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6687
- gi No. 2465008
- % Identity 70.5
- Alignment Length 315
- Location of Alignment in SEQ ID NO 756: from 1 to 309
  
- Alignment No. 6688
- gi No. 4056456
- % Identity 98.4
- Alignment Length 309
- Location of Alignment in SEQ ID NO 756: from 1 to 309

Maximum Length Sequence corresponding to clone ID 155209

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 757
- Ceres seq\_id 1498952

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 758
- Ceres seq\_id 1498953
- Location of start within SEQ ID NO 757: at 179 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6689
- Glycosyl hydrolases family 17
- Location within SEQ ID NO 758: from 33 to 231 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6690
- gi No. 2808438
- % Identity 71.4
- Alignment Length 227
- Location of Alignment in SEQ ID NO 758: from 5 to 231

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 759
- Ceres seq\_id 1498954
- Location of start within SEQ ID NO 757: at 428 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6691
- Glycosyl hydrolases family 17
- Location within SEQ ID NO 759: from 1 to 148 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6692
- gi No. 2808438
- % Identity 71.4
- Alignment Length 227
- Location of Alignment in SEQ ID NO 759: from 1 to 148

Maximum Length Sequence corresponding to clone ID 155438

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 760
- Ceres seq\_id 1498958

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 761
- Ceres seq\_id 1498959
- Location of start within SEQ ID NO 760: at 192 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6693
- gi No. 2088644
- % Identity 98.9
- Alignment Length 182
- Location of Alignment in SEQ ID NO 761: from 36 to 217

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 762
- Ceres seq\_id 1498960
- Location of start within SEQ ID NO 760: at 297 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6694
- gi No. 2088644
- % Identity 98.9
- Alignment Length 182
- Location of Alignment in SEQ ID NO 762: from 1 to 182

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 763
- Ceres seq\_id 1498961
- Location of start within SEQ ID NO 760: at 408 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6695
- gi No. 2088644
- % Identity 98.9
- Alignment Length 182
- Location of Alignment in SEQ ID NO 763: from 1 to 145

Maximum Length Sequence corresponding to clone ID 155456

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 764
- Ceres seq\_id 1498962

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 765
- Ceres seq\_id 1498963
- Location of start within SEQ ID NO 764: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6696
- Tropomyosins
- Location within SEQ ID NO 765: from 52 to 208 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6697
- gi No. 1946369
- % Identity 93.8
- Alignment Length 211
- Location of Alignment in SEQ ID NO 765: from 1 to 211

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 766
- Ceres seq\_id 1498964
- Location of start within SEQ ID NO 764: at 14 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6698
- Tropomyosins
- Location within SEQ ID NO 766: from 48 to 204 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6699
- gi No. 1946369
- % Identity 93.8
- Alignment Length 211
- Location of Alignment in SEQ ID NO 766: from 1 to 207

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 767
- Ceres seq\_id 1498965
- Location of start within SEQ ID NO 764: at 254 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6700
- Tropomyosins
- Location within SEQ ID NO 767: from 1 to 124 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6701
- gi No. 1946369
- % Identity 93.8
- Alignment Length 211
- Location of Alignment in SEQ ID NO 767: from 1 to 127

Maximum Length Sequence corresponding to clone ID 155628

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 768
- Ceres seq\_id 1498966

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 769
- Ceres seq\_id 1498967
- Location of start within SEQ ID NO 768: at 781 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6702

- S1 RNA binding domain
- Location within SEQ ID NO 769: from 84 to 153 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6703
- gi No. 2244822
- % Identity 100
- Alignment Length 161
- Location of Alignment in SEQ ID NO 769: from 18 to 178

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 770
- Ceres seq\_id 1498968
- Location of start within SEQ ID NO 768: at 814 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6704
- S1 RNA binding domain
- Location within SEQ ID NO 770: from 73 to 142 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6705
- gi No. 2244822
- % Identity 100
- Alignment Length 161
- Location of Alignment in SEQ ID NO 770: from 7 to 167

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 771
- Ceres seq\_id 1498969
- Location of start within SEQ ID NO 768: at 832 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6706
- S1 RNA binding domain
- Location within SEQ ID NO 771: from 67 to 136 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6707
- gi No. 2244822
- % Identity 100
- Alignment Length 161
- Location of Alignment in SEQ ID NO 771: from 1 to 161

Maximum Length Sequence corresponding to clone ID 155785

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 772
- Ceres seq\_id 1498970

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 773
- Ceres seq\_id 1498971
- Location of start within SEQ ID NO 772: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6708
- gi No. 4585997
- % Identity 92.6

- Alignment Length 231
- Location of Alignment in SEQ ID NO 773: from 1 to 230

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 774
- Ceres seq\_id 1498972
- Location of start within SEQ ID NO 772: at 14 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6709
- gi No. 4585997
- % Identity 92.6
- Alignment Length 231
- Location of Alignment in SEQ ID NO 774: from 1 to 226

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 775
- Ceres seq\_id 1498973
- Location of start within SEQ ID NO 772: at 302 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6710
- gi No. 4585997
- % Identity 92.6
- Alignment Length 231
- Location of Alignment in SEQ ID NO 775: from 1 to 130

Maximum Length Sequence corresponding to clone ID 155837

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 776
- Ceres seq\_id 1498974

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 777
- Ceres seq\_id 1498975
- Location of start within SEQ ID NO 776: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6711
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 777: from 59 to 104 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 778
- Ceres seq\_id 1498976
- Location of start within SEQ ID NO 776: at 13 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6712
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 778: from 55 to 100 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 779
- Ceres seq\_id 1498977
- Location of start within SEQ ID NO 776: at 148 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6713
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 779: from 10 to 55 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 155966

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 780
- Ceres seq\_id 1498978

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 781
- Ceres seq\_id 1498979
- Location of start within SEQ ID NO 780: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6714
- gi No. 2134207
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 781: from 92 to 102

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 782
- Ceres seq\_id 1498980
- Location of start within SEQ ID NO 780: at 63 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6715
- gi No. 4585983
- % Identity 98
- Alignment Length 98
- Location of Alignment in SEQ ID NO 782: from 1 to 98

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 783
- Ceres seq\_id 1498981
- Location of start within SEQ ID NO 780: at 527 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 156063

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 784
- Ceres seq\_id 1498982

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 785
- Ceres seq\_id 1498983



- Location of start within SEQ ID NO 784: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6716
- gi No. 4309726
- % Identity 88
- Alignment Length 337
- Location of Alignment in SEQ ID NO 785: from 74 to 381

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 786
- Ceres seq\_id 1498984
- Location of start within SEQ ID NO 784: at 505 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6717
- gi No. 4309726
- % Identity 88
- Alignment Length 337
- Location of Alignment in SEQ ID NO 786: from 1 to 213

Maximum Length Sequence corresponding to clone ID 156092

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 787
- Ceres seq\_id 1498985

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 788
- Ceres seq\_id 1498986
- Location of start within SEQ ID NO 787: at 367 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6718
- gi No. 3287693
- % Identity 86.3
- Alignment Length 481
- Location of Alignment in SEQ ID NO 788: from 3 to 482

- Alignment No. 6719
- gi No. 431164
- % Identity 78.5
- Alignment Length 356
- Location of Alignment in SEQ ID NO 788: from 1 to 350

- Alignment No. 6720
- gi No. 5123703
- % Identity 83.3
- Alignment Length 485
- Location of Alignment in SEQ ID NO 788: from 1 to 483

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 789
- Ceres seq\_id 1498987
- Location of start within SEQ ID NO 787: at 415 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6721
- gi No. 3287693
- % Identity 86.3
- Alignment Length 481
- Location of Alignment in SEQ ID NO 789: from 1 to 466
  
- Alignment No. 6722
- gi No. 431164
- % Identity 78.5
- Alignment Length 356
- Location of Alignment in SEQ ID NO 789: from 1 to 334
  
- Alignment No. 6723
- gi No. 5123703
- % Identity 83.3
- Alignment Length 485
- Location of Alignment in SEQ ID NO 789: from 1 to 467

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 790
- Ceres seq\_id 1498988
- Location of start within SEQ ID NO 787: at 451 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6724
- gi No. 3287693
- % Identity 86.3
- Alignment Length 481
- Location of Alignment in SEQ ID NO 790: from 1 to 454
  
- Alignment No. 6725
- gi No. 431164
- % Identity 78.5
- Alignment Length 356
- Location of Alignment in SEQ ID NO 790: from 1 to 322
  
- Alignment No. 6726
- gi No. 5123703
- % Identity 83.3
- Alignment Length 485
- Location of Alignment in SEQ ID NO 790: from 1 to 455

Maximum Length Sequence corresponding to clone ID 156222

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 791
- Ceres seq\_id 1498993

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 792
- Ceres seq\_id 1498994
- Location of start within SEQ ID NO 791: at 216 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6727
- gi No. 3935172

- % Identity 100
- Alignment Length 281
- Location of Alignment in SEQ ID NO 792: from 1 to 281
- Alignment No. 6728
- gi No. 3935173
- % Identity 84
- Alignment Length 282
- Location of Alignment in SEQ ID NO 792: from 1 to 281

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 793
- Ceres seq\_id 1498995
- Location of start within SEQ ID NO 791: at 228 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6729
- gi No. 3935172
- % Identity 100
- Alignment Length 281
- Location of Alignment in SEQ ID NO 793: from 1 to 277
- Alignment No. 6730
- gi No. 3935173
- % Identity 84
- Alignment Length 282
- Location of Alignment in SEQ ID NO 793: from 1 to 277

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 794
- Ceres seq\_id 1498996
- Location of start within SEQ ID NO 791: at 267 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6731
- gi No. 3935172
- % Identity 100
- Alignment Length 281
- Location of Alignment in SEQ ID NO 794: from 1 to 264
- Alignment No. 6732
- gi No. 3935173
- % Identity 84
- Alignment Length 282
- Location of Alignment in SEQ ID NO 794: from 1 to 264

Maximum Length Sequence corresponding to clone ID 156374

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 795
- Ceres seq\_id 1499001

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 796
- Ceres seq\_id 1499002
- Location of start within SEQ ID NO 795: at 236 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6733
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 796: from 131 to 382 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6734
- gi No. 4337195
- % Identity 87.1
- Alignment Length 413
- Location of Alignment in SEQ ID NO 796: from 1 to 412

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 797
- Ceres seq\_id 1499003
- Location of start within SEQ ID NO 795: at 350 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6735
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 797: from 93 to 344 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6736
- gi No. 4337195
- % Identity 87.1
- Alignment Length 413
- Location of Alignment in SEQ ID NO 797: from 1 to 374

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 798
- Ceres seq\_id 1499004
- Location of start within SEQ ID NO 795: at 365 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6737
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 798: from 88 to 339 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6738
- gi No. 4337195
- % Identity 87.1
- Alignment Length 413
- Location of Alignment in SEQ ID NO 798: from 1 to 369

Maximum Length Sequence corresponding to clone ID 156450

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 799
- Ceres seq\_id 1499009

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 800
- Ceres seq\_id 1499010
- Location of start within SEQ ID NO 799: at 90 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6739
- Tetrahydrofolate dehydrogenase/cyclohydrolase
- Location within SEQ ID NO 800: from 21 to 293 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6740
- gi No. 4103987
- % Identity 81
- Alignment Length 294
- Location of Alignment in SEQ ID NO 800: from 9 to 299

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 801
- Ceres seq\_id 1499011
- Location of start within SEQ ID NO 799: at 504 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6741
- Tetrahydrofolate dehydrogenase/cyclohydrolase
- Location within SEQ ID NO 801: from 1 to 155 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6742
- gi No. 4103987
- % Identity 81
- Alignment Length 294
- Location of Alignment in SEQ ID NO 801: from 1 to 161

Maximum Length Sequence corresponding to clone ID 156475

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 802
- Ceres seq\_id 1499012

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 803
- Ceres seq\_id 1499013
- Location of start within SEQ ID NO 802: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6743
- Semialdehyde dehydrogenase
- Location within SEQ ID NO 803: from 99 to 427 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6744
- gi No. 3687224
- % Identity 94.2
- Alignment Length 385
- Location of Alignment in SEQ ID NO 803: from 63 to 441

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 804
- Ceres seq\_id 1499014
- Location of start within SEQ ID NO 802: at 123 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6745
- Semialdehyde dehydrogenase
- Location within SEQ ID NO 804: from 59 to 387 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6746

- gi No. 3687224
- % Identity 94.2
- Alignment Length 385
- Location of Alignment in SEQ ID NO 804: from 23 to 401

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 805
- Ceres seq\_id 1499015
- Location of start within SEQ ID NO 802: at 249 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6747
- Semialdehyde dehydrogenase
- Location within SEQ ID NO 805: from 17 to 345 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6748
- gi No. 3687224
- % Identity 94.2
- Alignment Length 385
- Location of Alignment in SEQ ID NO 805: from 1 to 359

Maximum Length Sequence corresponding to clone ID 156655

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 806
- Ceres seq\_id 1499016

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 807
- Ceres seq\_id 1499017
- Location of start within SEQ ID NO 806: at 296 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6749
- Ezrin/radixin/moesin family
- Location within SEQ ID NO 807: from 80 to 286 aa.
- Alignment No. 6750
- Intermediate filament proteins
- Location within SEQ ID NO 807: from 11 to 284 aa.
- Alignment No. 6751
- Tropomyosins
- Location within SEQ ID NO 807: from 63 to 259 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 156972

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 808
- Ceres seq\_id 1499021

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 809
- Ceres seq\_id 1499022
- Location of start within SEQ ID NO 808: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6752

- gi No. 3785994
- % Identity 96.2
- Alignment Length 186
- Location of Alignment in SEQ ID NO 809: from 1 to 185

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 810
- Ceres seq\_id 1499023
- Location of start within SEQ ID NO 808: at 278 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6753
- gi No. 3785994
- % Identity 96.2
- Alignment Length 186
- Location of Alignment in SEQ ID NO 810: from 1 to 93

Maximum Length Sequence corresponding to clone ID 157034

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 811
- Ceres seq\_id 1499024

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 812
- Ceres seq\_id 1499025
- Location of start within SEQ ID NO 811: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6754
- Peroxidase
- Location within SEQ ID NO 812: from 154 to 273 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6755
- gi No. 1321627
- % Identity 74.2
- Alignment Length 424
- Location of Alignment in SEQ ID NO 812: from 28 to 442
  
- Alignment No. 6756
- gi No. 1369920
- % Identity 73.5
- Alignment Length 361
- Location of Alignment in SEQ ID NO 812: from 40 to 393
  
- Alignment No. 6757
- gi No. 1419390
- % Identity 99.5
- Alignment Length 426
- Location of Alignment in SEQ ID NO 812: from 27 to 452
  
- Alignment No. 6758
- gi No. 1805652
- % Identity 100
- Alignment Length 217
- Location of Alignment in SEQ ID NO 812: from 236 to 452
  
- Alignment No. 6759
- gi No. 1944507

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- % Identity 73.8
- Alignment Length 411
- Location of Alignment in SEQ ID NO 812: from 40 to 442

- Alignment No. 6760
- gi No. 2146725
- % Identity 72.6
- Alignment Length 423
- Location of Alignment in SEQ ID NO 812: from 27 to 442

- Alignment No. 6761
- gi No. 2392025
- % Identity 74
- Alignment Length 375
- Location of Alignment in SEQ ID NO 812: from 28 to 393

- Alignment No. 6762
- gi No. 2832920
- % Identity 73.6
- Alignment Length 411
- Location of Alignment in SEQ ID NO 812: from 40 to 442

- Alignment No. 6763
- gi No. 2832921
- % Identity 73.3
- Alignment Length 361
- Location of Alignment in SEQ ID NO 812: from 40 to 393

- Alignment No. 6764
- gi No. 3202024
- % Identity 70.5
- Alignment Length 366
- Location of Alignment in SEQ ID NO 812: from 28 to 393

- Alignment No. 6765
- gi No. 3202024
- % Identity 71.7
- Alignment Length 420
- Location of Alignment in SEQ ID NO 812: from 28 to 442

- Alignment No. 6766
- gi No. 3202026
- % Identity 70.5
- Alignment Length 366
- Location of Alignment in SEQ ID NO 812: from 28 to 393

- Alignment No. 6767
- gi No. 3202026
- % Identity 72
- Alignment Length 371
- Location of Alignment in SEQ ID NO 812: from 28 to 393

- Alignment No. 6768
- gi No. 4996602
- % Identity 74.4
- Alignment Length 437
- Location of Alignment in SEQ ID NO 812: from 17 to 442

- Alignment No. 6769
- gi No. 4996604
- % Identity 74.7

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- Alignment Length 388
- Location of Alignment in SEQ ID NO 812: from 17 to 393

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 813
- Ceres seq_id 1499026
- Location of start within SEQ ID NO 811: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6770
- Peroxidase
- Location within SEQ ID NO 813: from 128 to 247 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6771
- gi No. 1321627
- % Identity 74.2
- Alignment Length 424
- Location of Alignment in SEQ ID NO 813: from 2 to 416
- Alignment No. 6772
- gi No. 1369920
- % Identity 73.5
- Alignment Length 361
- Location of Alignment in SEQ ID NO 813: from 14 to 367
- Alignment No. 6773
- gi No. 1419390
- % Identity 99.5
- Alignment Length 426
- Location of Alignment in SEQ ID NO 813: from 1 to 426
- Alignment No. 6774
- gi No. 1805652
- % Identity 100
- Alignment Length 217
- Location of Alignment in SEQ ID NO 813: from 210 to 426
- Alignment No. 6775
- gi No. 1944507
- % Identity 73.8
- Alignment Length 411
- Location of Alignment in SEQ ID NO 813: from 14 to 416
- Alignment No. 6776
- gi No. 2146725
- % Identity 72.6
- Alignment Length 423
- Location of Alignment in SEQ ID NO 813: from 1 to 416
- Alignment No. 6777
- gi No. 2392025
- % Identity 74
- Alignment Length 375
- Location of Alignment in SEQ ID NO 813: from 2 to 367
- Alignment No. 6778
- gi No. 2832920
- % Identity 73.6
- Alignment Length 411

- Location of Alignment in SEQ ID NO 813: from 14 to 416
- Alignment No. 6779
- gi No. 2832921
- % Identity 73.3
- Alignment Length 361
- Location of Alignment in SEQ ID NO 813: from 14 to 367
- Alignment No. 6780
- gi No. 3202024
- % Identity 70.5
- Alignment Length 366
- Location of Alignment in SEQ ID NO 813: from 2 to 367
- Alignment No. 6781
- gi No. 3202024
- % Identity 71.7
- Alignment Length 420
- Location of Alignment in SEQ ID NO 813: from 2 to 416
- Alignment No. 6782
- gi No. 3202026
- % Identity 70.5
- Alignment Length 366
- Location of Alignment in SEQ ID NO 813: from 2 to 367
- Alignment No. 6783
- gi No. 3202026
- % Identity 72
- Alignment Length 371
- Location of Alignment in SEQ ID NO 813: from 2 to 367
- Alignment No. 6784
- gi No. 4996602
- % Identity 74.4
- Alignment Length 437
- Location of Alignment in SEQ ID NO 813: from 1 to 416
- Alignment No. 6785
- gi No. 4996604
- % Identity 74.7
- Alignment Length 388
- Location of Alignment in SEQ ID NO 813: from 1 to 367

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 814
- Ceres seq_id 1499027
- Location of start within SEQ ID NO 811: at 295 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6786
- Peroxidase
- Location within SEQ ID NO 814: from 56 to 175 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6787
- gi No. 1321627
- % Identity 74.2
- Alignment Length 424
- Location of Alignment in SEQ ID NO 814: from 1 to 344

- Alignment No. 6788
- gi No. 1369920
- % Identity 73.5
- Alignment Length 361
- Location of Alignment in SEQ ID NO 814: from 1 to 295

- Alignment No. 6789
- gi No. 1419390
- % Identity 99.5
- Alignment Length 426
- Location of Alignment in SEQ ID NO 814: from 1 to 354

- Alignment No. 6790
- gi No. 1805652
- % Identity 100
- Alignment Length 217
- Location of Alignment in SEQ ID NO 814: from 138 to 354

- Alignment No. 6791
- gi No. 1944507
- % Identity 73.8
- Alignment Length 411
- Location of Alignment in SEQ ID NO 814: from 1 to 344

- Alignment No. 6792
- gi No. 2146725
- % Identity 72.6
- Alignment Length 423
- Location of Alignment in SEQ ID NO 814: from 1 to 344

- Alignment No. 6793
- gi No. 2392025
- % Identity 74
- Alignment Length 375
- Location of Alignment in SEQ ID NO 814: from 1 to 295

- Alignment No. 6794
- gi No. 2832920
- % Identity 73.6
- Alignment Length 411
- Location of Alignment in SEQ ID NO 814: from 1 to 344

- Alignment No. 6795
- gi No. 2832921
- % Identity 73.3
- Alignment Length 361
- Location of Alignment in SEQ ID NO 814: from 1 to 295

- Alignment No. 6796
- gi No. 3202024
- % Identity 70.5
- Alignment Length 366
- Location of Alignment in SEQ ID NO 814: from 1 to 295

- Alignment No. 6797
- gi No. 3202024
- % Identity 71.7
- Alignment Length 420
- Location of Alignment in SEQ ID NO 814: from 1 to 344

- Alignment No. 6798
- gi No. 3202026
- % Identity 70.5
- Alignment Length 366
- Location of Alignment in SEQ ID NO 814: from 1 to 295

- Alignment No. 6799
- gi No. 3202026
- % Identity 72
- Alignment Length 371
- Location of Alignment in SEQ ID NO 814: from 1 to 295

- Alignment No. 6800
- gi No. 4996602
- % Identity 74.4
- Alignment Length 437
- Location of Alignment in SEQ ID NO 814: from 1 to 344

- Alignment No. 6801
- gi No. 4996604
- % Identity 74.7
- Alignment Length 388
- Location of Alignment in SEQ ID NO 814: from 1 to 295

Maximum Length Sequence corresponding to clone ID 157102

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 815
- Ceres seq_id 1499028

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 816
- Ceres seq_id 1499029
- Location of start within SEQ ID NO 815: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6802
- gi No. 3157941
- % Identity 84.1
- Alignment Length 207
- Location of Alignment in SEQ ID NO 816: from 4 to 67

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 817
- Ceres seq_id 1499030
- Location of start within SEQ ID NO 815: at 353 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6803
- gi No. 3157941
- % Identity 84.1
- Alignment Length 207
- Location of Alignment in SEQ ID NO 817: from 1 to 92

Maximum Length Sequence corresponding to clone ID 157110

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 818
- Ceres seq_id 1499031

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 819
- Ceres seq_id 1499032
- Location of start within SEQ ID NO 818: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6804
- gi No. 4895220
- % Identity 95.3
- Alignment Length 128
- Location of Alignment in SEQ ID NO 819: from 1 to 127

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 820
- Ceres seq_id 1499033
- Location of start within SEQ ID NO 818: at 264 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6805
- gi No. 4895220
- % Identity 95.3
- Alignment Length 128
- Location of Alignment in SEQ ID NO 820: from 1 to 40

Maximum Length Sequence corresponding to clone ID 157192

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 821
- Ceres seq_id 1499042

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 822
- Ceres seq_id 1499043
- Location of start within SEQ ID NO 821: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6806
- gi No. 5139335
- % Identity 99.8
- Alignment Length 444
- Location of Alignment in SEQ ID NO 822: from 11 to 454

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 823
- Ceres seq_id 1499044
- Location of start within SEQ ID NO 821: at 32 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6807
- gi No. 5139335
- % Identity 99.8
- Alignment Length 444
- Location of Alignment in SEQ ID NO 823: from 1 to 444

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 824

- Ceres seq_id 1499045
- Location of start within SEQ ID NO 821: at 83 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6808
- gi No. 5139335
- % Identity 99.8
- Alignment Length 444
- Location of Alignment in SEQ ID NO 824: from 1 to 427

Maximum Length Sequence corresponding to clone ID 157220

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 825
- Ceres seq_id 1499046

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 826
- Ceres seq_id 1499047
- Location of start within SEQ ID NO 825: at 177 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6809
- C2 domain
- Location within SEQ ID NO 826: from 83 to 158 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 827
- Ceres seq_id 1499048
- Location of start within SEQ ID NO 825: at 336 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6810
- C2 domain
- Location within SEQ ID NO 827: from 30 to 105 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 828
- Ceres seq_id 1499049
- Location of start within SEQ ID NO 825: at 531 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 157234

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 829
- Ceres seq_id 1499050

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 830
- Ceres seq_id 1499051
- Location of start within SEQ ID NO 829: at 111 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 6811
- Magnesium chelatase, subunit ChlI
- Location within SEQ ID NO 830: from 97 to 282 aa.

- Alignment No. 6812
- 60s Acidic ribosomal protein
- Location within SEQ ID NO 830: from 267 to 322 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6813
- gi No. 1173073
- % Identity 73.2
- Alignment Length 41
- Location of Alignment in SEQ ID NO 830: from 282 to 322

- Alignment No. 6814
- gi No. 1350779
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 830: from 295 to 322

- Alignment No. 6815
- gi No. 1710591
- % Identity 100
- Alignment Length 43
- Location of Alignment in SEQ ID NO 830: from 280 to 322

- Alignment No. 6816
- gi No. 2431767
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 830: from 283 to 322

- Alignment No. 6817
- gi No. 2431771
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 830: from 285 to 322

- Alignment No. 6818
- gi No. 3122752
- % Identity 71.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 830: from 282 to 322

- Alignment No. 6819
- gi No. 3135255
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 830: from 243 to 274

- Alignment No. 6820
- gi No. 3763970
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 830: from 296 to 322

- Alignment No. 6821
- gi No. 3860260

- % Identity 100
- Alignment Length 43
- Location of Alignment in SEQ ID NO 830: from 280 to 322

- Alignment No. 6822
- gi No. 3860261
- % Identity 97.7
- Alignment Length 43
- Location of Alignment in SEQ ID NO 830: from 280 to 322

- Alignment No. 6823
- gi No. 3913240
- % Identity 75.9
- Alignment Length 257
- Location of Alignment in SEQ ID NO 830: from 26 to 282

- Alignment No. 6824
- gi No. 4204372
- % Identity 72.1
- Alignment Length 43
- Location of Alignment in SEQ ID NO 830: from 280 to 322

- Alignment No. 6825
- gi No. 4204374
- % Identity 73.2
- Alignment Length 41
- Location of Alignment in SEQ ID NO 830: from 282 to 322

- Alignment No. 6826
- gi No. 4204376
- % Identity 79.1
- Alignment Length 43
- Location of Alignment in SEQ ID NO 830: from 280 to 322

- Alignment No. 6827
- gi No. 899610
- % Identity 73.2
- Alignment Length 41
- Location of Alignment in SEQ ID NO 830: from 282 to 322

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 831
- Ceres seq_id 1499052
- Location of start within SEQ ID NO 829: at 117 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6828
- Magnesium chelatase, subunit ChlI
- Location within SEQ ID NO 831: from 95 to 280 aa.

- Alignment No. 6829
- 60s Acidic ribosomal protein
- Location within SEQ ID NO 831: from 265 to 320 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6830
- gi No. 1173073
- % Identity 73.2
- Alignment Length 41
- Location of Alignment in SEQ ID NO 831: from 280 to 320

- Alignment No. 6831
- gi No. 1350779
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 831: from 293 to 320

- Alignment No. 6832
- gi No. 1710591
- % Identity 100
- Alignment Length 43
- Location of Alignment in SEQ ID NO 831: from 278 to 320

- Alignment No. 6833
- gi No. 2431767
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 831: from 281 to 320

- Alignment No. 6834
- gi No. 2431771
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 831: from 283 to 320

- Alignment No. 6835
- gi No. 3122752
- % Identity 71.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 831: from 280 to 320

- Alignment No. 6836
- gi No. 3135255
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 831: from 241 to 272

- Alignment No. 6837
- gi No. 3763970
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 831: from 294 to 320

- Alignment No. 6838
- gi No. 3860260
- % Identity 100
- Alignment Length 43
- Location of Alignment in SEQ ID NO 831: from 278 to 320

- Alignment No. 6839
- gi No. 3860261
- % Identity 97.7
- Alignment Length 43
- Location of Alignment in SEQ ID NO 831: from 278 to 320

- Alignment No. 6840
- gi No. 3913240
- % Identity 75.9
- Alignment Length 257
- Location of Alignment in SEQ ID NO 831: from 24 to 280

- Alignment No. 6841
- gi No. 4204372
- % Identity 72.1
- Alignment Length 43
- Location of Alignment in SEQ ID NO 831: from 278 to 320

- Alignment No. 6842
- gi No. 4204374
- % Identity 73.2
- Alignment Length 41
- Location of Alignment in SEQ ID NO 831: from 280 to 320

- Alignment No. 6843
- gi No. 4204376
- % Identity 79.1
- Alignment Length 43
- Location of Alignment in SEQ ID NO 831: from 278 to 320

- Alignment No. 6844
- gi No. 899610
- % Identity 73.2
- Alignment Length 41
- Location of Alignment in SEQ ID NO 831: from 280 to 320

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 832
- Ceres seq_id 1499053
- Location of start within SEQ ID NO 829: at 477 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6845
- Magnesium chelatase, subunit ChlI
- Location within SEQ ID NO 832: from 1 to 160 aa.

- Alignment No. 6846
- 60s Acidic ribosomal protein
- Location within SEQ ID NO 832: from 145 to 200 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6847
- gi No. 1173073
- % Identity 73.2
- Alignment Length 41
- Location of Alignment in SEQ ID NO 832: from 160 to 200

- Alignment No. 6848
- gi No. 1350779
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 832: from 173 to 200

- Alignment No. 6849
- gi No. 1710591
- % Identity 100
- Alignment Length 43
- Location of Alignment in SEQ ID NO 832: from 158 to 200

- Alignment No. 6850
- gi No. 2431767
- % Identity 71.1

- Alignment Length 45
- Location of Alignment in SEQ ID NO 832: from 161 to 200
- Alignment No. 6851
- gi No. 2431771
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 832: from 163 to 200
- Alignment No. 6852
- gi No. 3122752
- % Identity 71.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 832: from 160 to 200
- Alignment No. 6853
- gi No. 3135255
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 832: from 121 to 152
- Alignment No. 6854
- gi No. 3763970
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 832: from 174 to 200
- Alignment No. 6855
- gi No. 3860260
- % Identity 100
- Alignment Length 43
- Location of Alignment in SEQ ID NO 832: from 158 to 200
- Alignment No. 6856
- gi No. 3860261
- % Identity 97.7
- Alignment Length 43
- Location of Alignment in SEQ ID NO 832: from 158 to 200
- Alignment No. 6857
- gi No. 3913240
- % Identity 75.9
- Alignment Length 257
- Location of Alignment in SEQ ID NO 832: from 1 to 160
- Alignment No. 6858
- gi No. 4204372
- % Identity 72.1
- Alignment Length 43
- Location of Alignment in SEQ ID NO 832: from 158 to 200
- Alignment No. 6859
- gi No. 4204374
- % Identity 73.2
- Alignment Length 41
- Location of Alignment in SEQ ID NO 832: from 160 to 200
- Alignment No. 6860
- gi No. 4204376
- % Identity 79.1
- Alignment Length 43

- Location of Alignment in SEQ ID NO 832: from 158 to 200
- Alignment No. 6861
- gi No. 899610
- % Identity 73.2
- Alignment Length 41
- Location of Alignment in SEQ ID NO 832: from 160 to 200

Maximum Length Sequence corresponding to clone ID 157460

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 833
- Ceres seq_id 1499054

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 834
- Ceres seq_id 1499055
- Location of start within SEQ ID NO 833: at 201 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6862
- gi No. 4249416
- % Identity 98.9
- Alignment Length 89
- Location of Alignment in SEQ ID NO 834: from 25 to 112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 835
- Ceres seq_id 1499056
- Location of start within SEQ ID NO 833: at 273 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6863
- gi No. 4249416
- % Identity 98.9
- Alignment Length 89
- Location of Alignment in SEQ ID NO 835: from 1 to 88

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 836
- Ceres seq_id 1499057
- Location of start within SEQ ID NO 833: at 306 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6864
- gi No. 4249416
- % Identity 98.9
- Alignment Length 89
- Location of Alignment in SEQ ID NO 836: from 1 to 77

Maximum Length Sequence corresponding to clone ID 157614

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 837
- Ceres seq_id 1499066

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 838
- Ceres seq_id 1499067

- Location of start within SEQ ID NO 837: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6865
- gi No. 2252829
- % Identity 97.8
- Alignment Length 364
- Location of Alignment in SEQ ID NO 838: from 34 to 397
- Alignment No. 6866
- gi No. 4508074
- % Identity 71.4
- Alignment Length 390
- Location of Alignment in SEQ ID NO 838: from 34 to 397

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 839
- Ceres seq_id 1499068
- Location of start within SEQ ID NO 837: at 100 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6867
- gi No. 2252829
- % Identity 97.8
- Alignment Length 364
- Location of Alignment in SEQ ID NO 839: from 1 to 364
- Alignment No. 6868
- gi No. 4508074
- % Identity 71.4
- Alignment Length 390
- Location of Alignment in SEQ ID NO 839: from 1 to 364

Maximum Length Sequence corresponding to clone ID 157665

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 840
- Ceres seq_id 1499073

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 841
- Ceres seq_id 1499074
- Location of start within SEQ ID NO 840: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6869
- gi No. 4006917
- % Identity 100
- Alignment Length 281
- Location of Alignment in SEQ ID NO 841: from 152 to 432

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 842
- Ceres seq_id 1499075
- Location of start within SEQ ID NO 840: at 90 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6870
- gi No. 4006917
- % Identity 100
- Alignment Length 281
- Location of Alignment in SEQ ID NO 842: from 123 to 403

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 843
- Ceres seq_id 1499076
- Location of start within SEQ ID NO 840: at 654 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6871
- gi No. 4006917
- % Identity 100
- Alignment Length 281
- Location of Alignment in SEQ ID NO 843: from 1 to 215

Maximum Length Sequence corresponding to clone ID 157706

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 844
- Ceres seq_id 1499077

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 845
- Ceres seq_id 1499078
- Location of start within SEQ ID NO 844: at 21 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 6872
- F-box domain.
- Location within SEQ ID NO 845: from 59 to 105 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6873
- gi No. 3298544
- % Identity 100
- Alignment Length 227
- Location of Alignment in SEQ ID NO 845: from 60 to 286
- Alignment No. 6874
- gi No. 3298545
- % Identity 100
- Alignment Length 42
- Location of Alignment in SEQ ID NO 845: from 330 to 371
- Alignment No. 6875
- gi No. 3426041
- % Identity 80.6
- Alignment Length 62
- Location of Alignment in SEQ ID NO 845: from 311 to 371
- Alignment No. 6876
- gi No. 3426041
- % Identity 80.7
- Alignment Length 285

- Location of Alignment in SEQ ID NO 845: from 1 to 285

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 846
- Ceres seq_id 1499079
- Location of start within SEQ ID NO 844: at 144 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6877
- F-box domain.
- Location within SEQ ID NO 846: from 18 to 64 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6878
- gi No. 3298544
- % Identity 100
- Alignment Length 227
- Location of Alignment in SEQ ID NO 846: from 19 to 245
- Alignment No. 6879
- gi No. 3298545
- % Identity 100
- Alignment Length 42
- Location of Alignment in SEQ ID NO 846: from 289 to 330
- Alignment No. 6880
- gi No. 3426041
- % Identity 80.6
- Alignment Length 62
- Location of Alignment in SEQ ID NO 846: from 270 to 330
- Alignment No. 6881
- gi No. 3426041
- % Identity 80.7
- Alignment Length 285
- Location of Alignment in SEQ ID NO 846: from 1 to 244

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 847
- Ceres seq_id 1499080
- Location of start within SEQ ID NO 844: at 198 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6882
- F-box domain.
- Location within SEQ ID NO 847: from 1 to 46 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6883
- gi No. 3298544
- % Identity 100
- Alignment Length 227
- Location of Alignment in SEQ ID NO 847: from 1 to 227
- Alignment No. 6884
- gi No. 3298545
- % Identity 100
- Alignment Length 42
- Location of Alignment in SEQ ID NO 847: from 271 to 312

- Alignment No. 6885
- gi No. 3426041
- % Identity 80.6
- Alignment Length 62
- Location of Alignment in SEQ ID NO 847: from 252 to 312

- Alignment No. 6886
- gi No. 3426041
- % Identity 80.7
- Alignment Length 285
- Location of Alignment in SEQ ID NO 847: from 1 to 226

Maximum Length Sequence corresponding to clone ID 157714

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 848
- Ceres seq_id 1499085

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 849
- Ceres seq_id 1499086
- Location of start within SEQ ID NO 848: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6887
- Dehydrins
- Location within SEQ ID NO 849: from 37 to 94 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6888
- gi No. 1169278
- % Identity 74
- Alignment Length 50
- Location of Alignment in SEQ ID NO 849: from 36 to 85

- Alignment No. 6889
- gi No. 1169280
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 849: from 36 to 94

- Alignment No. 6890
- gi No. 2129637
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 849: from 36 to 94

- Alignment No. 6891
- gi No. 99681
- % Identity 87.9
- Alignment Length 141
- Location of Alignment in SEQ ID NO 849: from 7 to 94

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 850
- Ceres seq_id 1499087
- Location of start within SEQ ID NO 848: at 108 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6892

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- Dehydrins
- Location within SEQ ID NO 850: from 2 to 59 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6893
- gi No. 1169278
- % Identity 74
- Alignment Length 50
- Location of Alignment in SEQ ID NO 850: from 1 to 50
- Alignment No. 6894
- gi No. 1169280
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 850: from 1 to 59
- Alignment No. 6895
- gi No. 2129637
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 850: from 1 to 59
- Alignment No. 6896
- gi No. 99681
- % Identity 87.9
- Alignment Length 141
- Location of Alignment in SEQ ID NO 850: from 1 to 59

Maximum Length Sequence corresponding to clone ID 157735

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 851
- Ceres seq_id 1499088

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 852
- Ceres seq_id 1499089
- Location of start within SEQ ID NO 851: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6897
- Monooxygenase
- Location within SEQ ID NO 852: from 2 to 91 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6898
- gi No. 2804278
- % Identity 78.6
- Alignment Length 206
- Location of Alignment in SEQ ID NO 852: from 2 to 207
- Alignment No. 6899
- gi No. 3445200
- % Identity 76.5
- Alignment Length 204
- Location of Alignment in SEQ ID NO 852: from 2 to 205
- Alignment No. 6900
- gi No. 4490721
- % Identity 75.6
- Alignment Length 205
- Location of Alignment in SEQ ID NO 852: from 2 to 206

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(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 853
- Ceres seq_id 1499090
- Location of start within SEQ ID NO 851: at 27 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6901
- Monooxygenase
- Location within SEQ ID NO 853: from 1 to 83 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6902
- gi No. 2804278
- % Identity 78.6
- Alignment Length 206
- Location of Alignment in SEQ ID NO 853: from 1 to 199
- Alignment No. 6903
- gi No. 3445200
- % Identity 76.5
- Alignment Length 204
- Location of Alignment in SEQ ID NO 853: from 1 to 197
- Alignment No. 6904
- gi No. 4490721
- % Identity 75.6
- Alignment Length 205
- Location of Alignment in SEQ ID NO 853: from 1 to 198

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 854
- Ceres seq_id 1499091
- Location of start within SEQ ID NO 851: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6905
- Monooxygenase
- Location within SEQ ID NO 854: from 1 to 78 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6906
- gi No. 2804278
- % Identity 78.6
- Alignment Length 206
- Location of Alignment in SEQ ID NO 854: from 1 to 194
- Alignment No. 6907
- gi No. 3445200
- % Identity 76.5
- Alignment Length 204
- Location of Alignment in SEQ ID NO 854: from 1 to 192
- Alignment No. 6908
- gi No. 4490721
- % Identity 75.6
- Alignment Length 205
- Location of Alignment in SEQ ID NO 854: from 1 to 193

(A) Polynucleotide Sequence

- (B) Polypeptide Sequence

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- #### (D) Related Amino Acid Sequences

- ```
- Alignment No. 6911
- gi No. 1168251
- % Identity 85.8
- Alignment Length 169
- Location of Alignment in SEQ ID NO 856: from 74 to 242
```

- ```
- Alignment No. 6912
- gi No. 1172872
- % Identity 97.7
- Alignment Length 173
- Location of Alignment in SEQ ID NO 856: from 74 to 246
```

- ```
- Alignment No. 6913
- gi No. 118150
- % Identity 74
- Alignment Length 170
- Location of Alignment in SEQ ID NO 856: from 74 to 242
```

- Alignment No. 6914
- gi No. 129613
- % Identity 87.5
- Alignment Length 96
- Location of Alignment in SEQ ID NO 856: from 150 to 245

- ```
- Alignment No. 6915
- gi No. 1401242
- % Identity 74
- Alignment Length 170
- Location of Alignment in SEQ ID NO 856: from 74 to 242
```

- ```
- Alignment No. 6916
- gi No. 1527225
- % Identity 90.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 856: from 151 to 234
```

- ```
- Alignment No. 6917
- gi No. 1619903
- % Identity 72.8
```

No.	Name	Age	Sex	Religion	Marital Status	Occupation	Income	Assets	Liabilities	Net Worth	Comments
1	John Doe	45	M	Protestant	Married	Teacher	\$12,000	\$15,000	\$5,000	\$10,000	Stable income, good assets.
2	Jane Smith	38	F	Catholic	Single	Nurse	\$10,000	\$12,000	\$2,000	\$8,000	Good income, moderate assets.
3	Robert Brown	52	M	Jewish	Married	Engineer	\$15,000	\$20,000	\$8,000	\$12,000	High income, excellent assets.
4	Mary White	41	F	Methodist	Married	Homemaker	\$8,000	\$10,000	\$3,000	\$7,000	Low income, good assets.
5	William Black	35	M	Buddhist	Single	Software Developer	\$18,000	\$25,000	\$10,000	\$15,000	High income, excellent assets.
6	Elizabeth Green	48	F	Anglican	Married	Librarian	\$9,000	\$11,000	\$4,000	\$7,000	Stable income, good assets.
7	James Taylor	55	M	Muslim	Married	Retired	\$11,000	\$14,000	\$6,000	\$8,000	Stable income, good assets.
8	Sarah Johnson	33	F	Hindu	Single	Marketing Executive	\$16,000	\$22,000	\$9,000	\$13,000	High income, excellent assets.
9	Michael Davis	42	M	Sikh	Married	Accountant	\$13,000	\$16,000	\$7,000	\$9,000	Stable income, good assets.
10	Linda Wilson	39	F	Orthodox	Married	Teacher	\$10,000	\$13,000	\$5,000	\$8,000	Stable income, good assets.

- Alignment Length 173
- Location of Alignment in SEQ ID NO 856: from 74 to 246
- Alignment No. 6918
- gi No. 1706260
- % Identity 76.7
- Alignment Length 164
- Location of Alignment in SEQ ID NO 856: from 79 to 239
- Alignment No. 6919
- gi No. 2118130
- % Identity 77.4
- Alignment Length 138
- Location of Alignment in SEQ ID NO 856: from 105 to 239
- Alignment No. 6920
- gi No. 2244977
- % Identity 74.9
- Alignment Length 167
- Location of Alignment in SEQ ID NO 856: from 74 to 239
- Alignment No. 6921
- gi No. 2253415
- % Identity 76.5
- Alignment Length 166
- Location of Alignment in SEQ ID NO 856: from 74 to 239
- Alignment No. 6922
- gi No. 2511691
- % Identity 77.2
- Alignment Length 171
- Location of Alignment in SEQ ID NO 856: from 74 to 244
- Alignment No. 6923
- gi No. 3377952
- % Identity 76.5
- Alignment Length 167
- Location of Alignment in SEQ ID NO 856: from 74 to 239
- Alignment No. 6924
- gi No. 419781
- % Identity 71.2
- Alignment Length 170
- Location of Alignment in SEQ ID NO 856: from 74 to 243
- Alignment No. 6925
- gi No. 419782
- % Identity 73.2
- Alignment Length 168
- Location of Alignment in SEQ ID NO 856: from 76 to 243
- Alignment No. 6926
- gi No. 4567274
- % Identity 85.8
- Alignment Length 169
- Location of Alignment in SEQ ID NO 856: from 74 to 242
- Alignment No. 6927
- gi No. 4757570
- % Identity 75.6
- Alignment Length 164

- Location of Alignment in SEQ ID NO 856: from 80 to 243
- Alignment No. 6928
- gi No. 5051468
- % Identity 72.4
- Alignment Length 170
- Location of Alignment in SEQ ID NO 856: from 74 to 243
- Alignment No. 6929
- gi No. 542004
- % Identity 74.6
- Alignment Length 170
- Location of Alignment in SEQ ID NO 856: from 74 to 242

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 857
- Ceres seq_id 1499094
- Location of start within SEQ ID NO 855: at 352 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6930
- Papain family cysteine protease
- Location within SEQ ID NO 857: from 53 to 217 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6931
- gi No. 100203
- % Identity 70
- Alignment Length 170
- Location of Alignment in SEQ ID NO 857: from 53 to 222
- Alignment No. 6932
- gi No. 1168251
- % Identity 85.8
- Alignment Length 169
- Location of Alignment in SEQ ID NO 857: from 53 to 221
- Alignment No. 6933
- gi No. 1172872
- % Identity 97.7
- Alignment Length 173
- Location of Alignment in SEQ ID NO 857: from 53 to 225
- Alignment No. 6934
- gi No. 118150
- % Identity 74
- Alignment Length 170
- Location of Alignment in SEQ ID NO 857: from 53 to 221
- Alignment No. 6935
- gi No. 129613
- % Identity 87.5
- Alignment Length 96
- Location of Alignment in SEQ ID NO 857: from 129 to 224
- Alignment No. 6936
- gi No. 1401242
- % Identity 74
- Alignment Length 170
- Location of Alignment in SEQ ID NO 857: from 53 to 221

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- Alignment No. 6937
- gi No. 1527225
- % Identity 90.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 857: from 130 to 213

- Alignment No. 6938
- gi No. 1619903
- % Identity 72.8
- Alignment Length 173
- Location of Alignment in SEQ ID NO 857: from 53 to 225

- Alignment No. 6939
- gi No. 1706260
- % Identity 76.7
- Alignment Length 164
- Location of Alignment in SEQ ID NO 857: from 58 to 218

- Alignment No. 6940
- gi No. 2118130
- % Identity 77.4
- Alignment Length 138
- Location of Alignment in SEQ ID NO 857: from 84 to 218

- Alignment No. 6941
- gi No. 2244977
- % Identity 74.9
- Alignment Length 167
- Location of Alignment in SEQ ID NO 857: from 53 to 218

- Alignment No. 6942
- gi No. 2253415
- % Identity 76.5
- Alignment Length 166
- Location of Alignment in SEQ ID NO 857: from 53 to 218

- Alignment No. 6943
- gi No. 2511691
- % Identity 77.2
- Alignment Length 171
- Location of Alignment in SEQ ID NO 857: from 53 to 223

- Alignment No. 6944
- gi No. 3377952
- % Identity 76.5
- Alignment Length 167
- Location of Alignment in SEQ ID NO 857: from 53 to 218

- Alignment No. 6945
- gi No. 419781
- % Identity 71.2
- Alignment Length 170
- Location of Alignment in SEQ ID NO 857: from 53 to 222

- Alignment No. 6946
- gi No. 419782
- % Identity 73.2
- Alignment Length 168
- Location of Alignment in SEQ ID NO 857: from 55 to 222

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- Alignment No. 6947
- gi No. 4567274
- % Identity 85.8
- Alignment Length 169
- Location of Alignment in SEQ ID NO 857: from 53 to 221

- Alignment No. 6948
- gi No. 4757570
- % Identity 75.6
- Alignment Length 164
- Location of Alignment in SEQ ID NO 857: from 59 to 222

- Alignment No. 6949
- gi No. 5051468
- % Identity 72.4
- Alignment Length 170
- Location of Alignment in SEQ ID NO 857: from 53 to 222

- Alignment No. 6950
- gi No. 542004
- % Identity 74.6
- Alignment Length 170
- Location of Alignment in SEQ ID NO 857: from 53 to 221

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 858
- Ceres seq_id 1499095
- Location of start within SEQ ID NO 855: at 553 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6951
- Papain family cysteine protease
- Location within SEQ ID NO 858: from 1 to 150 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6952
- gi No. 100203
- % Identity 70
- Alignment Length 170
- Location of Alignment in SEQ ID NO 858: from 1 to 155

- Alignment No. 6953
- gi No. 1168251
- % Identity 85.8
- Alignment Length 169
- Location of Alignment in SEQ ID NO 858: from 1 to 154

- Alignment No. 6954
- gi No. 1172872
- % Identity 97.7
- Alignment Length 173
- Location of Alignment in SEQ ID NO 858: from 1 to 158

- Alignment No. 6955
- gi No. 118150
- % Identity 74
- Alignment Length 170
- Location of Alignment in SEQ ID NO 858: from 1 to 154

- Alignment No. 6956

- gi No. 129613
- % Identity 87.5
- Alignment Length 96
- Location of Alignment in SEQ ID NO 858: from 62 to 157

- Alignment No. 6957
- gi No. 1401242
- % Identity 74
- Alignment Length 170
- Location of Alignment in SEQ ID NO 858: from 1 to 154

- Alignment No. 6958
- gi No. 1527225
- % Identity 90.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 858: from 63 to 146

- Alignment No. 6959
- gi No. 1619903
- % Identity 72.8
- Alignment Length 173
- Location of Alignment in SEQ ID NO 858: from 1 to 158

- Alignment No. 6960
- gi No. 1706260
- % Identity 76.7
- Alignment Length 164
- Location of Alignment in SEQ ID NO 858: from 1 to 151

- Alignment No. 6961
- gi No. 2118130
- % Identity 77.4
- Alignment Length 138
- Location of Alignment in SEQ ID NO 858: from 17 to 151

- Alignment No. 6962
- gi No. 2244977
- % Identity 74.9
- Alignment Length 167
- Location of Alignment in SEQ ID NO 858: from 1 to 151

- Alignment No. 6963
- gi No. 2253415
- % Identity 76.5
- Alignment Length 166
- Location of Alignment in SEQ ID NO 858: from 1 to 151

- Alignment No. 6964
- gi No. 2511691
- % Identity 77.2
- Alignment Length 171
- Location of Alignment in SEQ ID NO 858: from 1 to 156

- Alignment No. 6965
- gi No. 3377952
- % Identity 76.5
- Alignment Length 167
- Location of Alignment in SEQ ID NO 858: from 1 to 151

- Alignment No. 6966
- gi No. 419781

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- % Identity 71.2
- Alignment Length 170
- Location of Alignment in SEQ ID NO 858: from 1 to 155

- Alignment No. 6967
- gi No. 419782
- % Identity 73.2
- Alignment Length 168
- Location of Alignment in SEQ ID NO 858: from 1 to 155

- Alignment No. 6968
- gi No. 4567274
- % Identity 85.8
- Alignment Length 169
- Location of Alignment in SEQ ID NO 858: from 1 to 154

- Alignment No. 6969
- gi No. 4757570
- % Identity 75.6
- Alignment Length 164
- Location of Alignment in SEQ ID NO 858: from 1 to 155

- Alignment No. 6970
- gi No. 5051468
- % Identity 72.4
- Alignment Length 170
- Location of Alignment in SEQ ID NO 858: from 1 to 155

- Alignment No. 6971
- gi No. 542004
- % Identity 74.6
- Alignment Length 170
- Location of Alignment in SEQ ID NO 858: from 1 to 154

Maximum Length Sequence corresponding to clone ID 158028

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 859
- Ceres seq_id 1499100

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 860
- Ceres seq_id 1499101
- Location of start within SEQ ID NO 859: at 112 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6972
- gi No. 5123566
- % Identity 100
- Alignment Length 533
- Location of Alignment in SEQ ID NO 860: from 1 to 533

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 861
- Ceres seq_id 1499102
- Location of start within SEQ ID NO 859: at 151 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6973

- gi No. 5123566
- % Identity 100
- Alignment Length 533
- Location of Alignment in SEQ ID NO 861: from 1 to 520

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 862
- Ceres seq_id 1499103
- Location of start within SEQ ID NO 859: at 283 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 6974
- gi No. 5123566
- % Identity 100
- Alignment Length 533
- Location of Alignment in SEQ ID NO 862: from 1 to 476

Maximum Length Sequence corresponding to clone ID 158108

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 863
- Ceres seq_id 1499108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 864
- Ceres seq_id 1499109
- Location of start within SEQ ID NO 863: at 60 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6975
- Cytochrome P450
- Location within SEQ ID NO 864: from 37 to 499 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6976
- gi No. 3128210
- % Identity 82.1
- Alignment Length 498
- Location of Alignment in SEQ ID NO 864: from 1 to 498

- Alignment No. 6977
- gi No. 3128211
- % Identity 99.8
- Alignment Length 499
- Location of Alignment in SEQ ID NO 864: from 1 to 499

- Alignment No. 6978
- gi No. 3927832
- % Identity 74
- Alignment Length 497
- Location of Alignment in SEQ ID NO 864: from 1 to 497

- Alignment No. 6979
- gi No. 3927833
- % Identity 73.6
- Alignment Length 497
- Location of Alignment in SEQ ID NO 864: from 1 to 497

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 865

- Ceres seq_id 1499110
- Location of start within SEQ ID NO 863: at 528 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6980
- Cytochrome P450
- Location within SEQ ID NO 865: from 1 to 343 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6981
- gi No. 3128210
- % Identity 82.1
- Alignment Length 498
- Location of Alignment in SEQ ID NO 865: from 1 to 342
- Alignment No. 6982
- gi No. 3128211
- % Identity 99.8
- Alignment Length 499
- Location of Alignment in SEQ ID NO 865: from 1 to 343
- Alignment No. 6983
- gi No. 3927832
- % Identity 74
- Alignment Length 497
- Location of Alignment in SEQ ID NO 865: from 1 to 341
- Alignment No. 6984
- gi No. 3927833
- % Identity 73.6
- Alignment Length 497
- Location of Alignment in SEQ ID NO 865: from 1 to 341

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 866
- Ceres seq_id 1499111
- Location of start within SEQ ID NO 863: at 588 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6985
- Cytochrome P450
- Location within SEQ ID NO 866: from 1 to 323 aa.

(D) Related Amino Acid Sequences

- Alignment No. 6986
- gi No. 3128210
- % Identity 82.1
- Alignment Length 498
- Location of Alignment in SEQ ID NO 866: from 1 to 322
- Alignment No. 6987
- gi No. 3128211
- % Identity 99.8
- Alignment Length 499
- Location of Alignment in SEQ ID NO 866: from 1 to 323
- Alignment No. 6988
- gi No. 3927832
- % Identity 74

- ```
- Alignment Length 497
- Location of Alignment in SEQ ID NO 866: from 1 to 321

- Alignment No. 6989
- gi No. 3927833
- % Identity 73.6
- Alignment Length 497
- Location of Alignment in SEQ ID NO 866: from 1 to 321
```

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 867  
- Ceres seq id 1499112

- Pat. Appln. SEQ ID NO 868

- Ceres seq\_id 1499113
- Location of start within SEQ ID NO 867: at 27 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6990

- ```
- gi No. 5123937
- % Identity 100
- Alignment Length 84
- Location of Alignment in SEQ ID NO 868: from 1 to 84
```

- Pat. Appln. SEQ ID NO 869

- Ceres seq_id 1499114
- Location of start within SEQ ID NO 867: at 886 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6991

- ```
- gi No. 4586265
- % Identity 81
- Alignment Length 79
- Location of Alignment in SEQ ID NO 869: from 20 to 98
```

- ```
- Alignment No. 6992
- gi No. 5123937
- % Identity 97
- Alignment Length 133
- Location of Alignment in SEQ ID NO 869: from 19 to 151
```

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 870
- Ceres seq id 1499115

- Pat. Appln. SEQ ID NO 871

- Ceres seq_id 1499116
- Location of start within SEQ ID NO 870: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6993
- Amino acid permease
- Location within SEQ ID NO 871: from 69 to 488 aa.

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	21	55
Gender	0.5	0.5	0	1
Marital Status	0.7	0.5	0	1
Education	12.5	1.5	9	16
Income	15000	5000	5000	30000
Health	0.8	0.4	0	1
Smoking	0.3	0.5	0	1
Drinking	0.2	0.4	0	1
Exercise	0.6	0.5	0	1
Stress	0.7	0.5	0	1
Sleep	0.8	0.4	0	1
Work	0.9	0.3	0	1
Family	0.7	0.5	0	1
Friends	0.6	0.5	0	1
Community	0.5	0.5	0	1
Society	0.4	0.5	0	1
Nature	0.3	0.5	0	1
Art	0.2	0.4	0	1
Music	0.1	0.3	0	1
Reading	0.0	0.2	0	1
Travel	0.0	0.1	0	1
Volunteering	0.0	0.1	0	1
Philosophy	0.0	0.1	0	1
Religion	0.0	0.1	0	1
Politics	0.0	0.1	0	1
Science	0.0	0.1	0	1
History	0.0	0.1	0	1
Geography	0.0	0.1	0	1
Language	0.0	0.1	0	1
Mathematics	0.0	0.1	0	1
Physics	0.0	0.1	0	1
Chemistry	0.0	0.1	0	1
Biology	0.0	0.1	0	1
Medicine	0.0	0.1	0	1
Law	0.0	0.1	0	1
Business	0.0	0.1	0	1
Engineering	0.0	0.1	0	1
Architecture	0.0	0.1	0	1
Design	0.0	0.1	0	1
Writing	0.0	0.1	0	1
Acting	0.0	0.1	0	1
Dancing	0.0	0.1	0	1
Sports	0.0	0.1	0	1
Gardening	0.0	0.1	0	1
Cooking	0.0	0.1	0	1
Shopping	0.0	0.1	0	1
Traveling	0.0	0.1	0	1
Volunteering	0.0	0.1	0	1
Philosophy	0.0	0.1	0	1
Religion	0.0	0.1	0	1
Politics	0.0	0.1	0	1
Science	0.0	0.1	0	1
History	0.0	0.1	0	1
Geography	0.0	0.1	0	1
Language	0.0	0.1	0	1
Mathematics	0.0	0.1	0	1
Physics	0.0	0.1	0	1
Chemistry	0.0	0.1	0	1
Biology	0.0	0.1	0	1
Medicine	0.0	0.1	0	1
Law	0.0	0.1	0	1
Business	0.0	0.1	0	1
Engineering	0.0	0.1	0	1
Architecture	0.0	0.1	0	1
Design	0.0	0.1	0	1
Writing	0.0	0.1	0	1
Acting	0.0	0.1	0	1
Dancing	0.0	0.1	0	1
Sports	0.0	0.1	0	1
Gardening	0.0	0.1	0	1
Cooking	0.0	0.1	0	1
Shopping	0.0	0.1	0	1
Traveling	0.0	0.1	0	1
Volunteering	0.0	0.1	0	1
Philosophy	0.0	0.1	0	1
Religion	0.0	0.1	0	1
Politics	0.0	0.1	0	1
Science	0.0	0.1	0	1
History	0.0	0.1	0	1
Geography	0.0	0.1	0	1
Language	0.0	0.1	0	1
Mathematics	0.0	0.1	0	1
Physics	0.0	0.1	0	1
Chemistry	0.0	0.1	0	1
Biology	0.0	0.1	0	1
Medicine	0.0	0.1	0	1
Law	0.0	0.1		

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 872
- Ceres seq_id 1499117
- Location of start within SEQ ID NO 870: at 39 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6994
- Amino acid permease
- Location within SEQ ID NO 872: from 57 to 476 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 873
- Ceres seq_id 1499118
- Location of start within SEQ ID NO 870: at 174 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6995
- Amino acid permease
- Location within SEQ ID NO 873: from 12 to 431 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 158178

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 874
- Ceres seq_id 1499119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 875
- Ceres seq_id 1499120
- Location of start within SEQ ID NO 874: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6996
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 875: from 42 to 194 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 876
- Ceres seq_id 1499121
- Location of start within SEQ ID NO 874: at 39 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6997
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 876: from 30 to 182 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 877

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6998
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 877: from 26 to 178 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 158184

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 878
- Ceres seq id 1499123

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 879
- Ceres seq_id 1499124
- Location of start within SEQ ID NO 878: at 1 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 6999
- Dehydrogenase El component
- Location within SEQ ID NO 879: from 127 to 412 aa.

#### (D) Related Amino Acid Sequences

- ```
- Alignment No. 7000
- gi No. 2454182
- % Identity 100
- Alignment Length 374
- Location of Alignment in SEQ ID NO 879: from 39 to 412
```

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 880
- Ceres seq_id 1499125
- Location of start within SEQ ID NO 878: at 115 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 7001
- Dehydrogenase E1 component
- Location within SEQ ID NO 880: from 89 to 374 aa.

#### (D) Related Amino Acid Sequences

- ```
- Alignment No. 7002
- gi No. 2454182
- % Identity 100
- Alignment Length 374
- Location of Alignment in SEQ ID NO 880: from 1 to 374
```

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 881
- Ceres seq_id 1499126
- Location of start within SEQ ID NO 878: at 385 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 7003
- Dehydrogenase El component
- Location within SEQ ID NO 881: from 1 to 284 aa.

(D) Related Amino Acid Sequences

- Alignment No. 7004
- gi No. 2454182
- % Identity 100
- Alignment Length 374
- Location of Alignment in SEQ ID NO 881: from 1 to 284

Maximum Length Sequence corresponding to clone ID 158231

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 882
- Ceres seq\_id 1499127

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 883
- Ceres seq\_id 1499128
- Location of start within SEQ ID NO 882: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 7005
- Kelch motif
- Location within SEQ ID NO 883: from 9 to 49 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 884
- Ceres seq\_id 1499129
- Location of start within SEQ ID NO 882: at 7 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 7006
- Kelch motif
- Location within SEQ ID NO 884: from 7 to 47 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 885
- Ceres seq\_id 1499130
- Location of start within SEQ ID NO 882: at 103 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 158240

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 886
- Ceres seq\_id 1499135

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 887
- Ceres seq\_id 1499136
- Location of start within SEQ ID NO 886: at 137 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 7007
- AP2 domain
- Location within SEQ ID NO 887: from 125 to 186 aa.

(D) Related Amino Acid Sequences

- Alignment No. 7008
- gi No. 1208497
- % Identity 74.6
- Alignment Length 63
- Location of Alignment in SEQ ID NO 887: from 125 to 186
  
- Alignment No. 7009
- gi No. 2213612
- % Identity 70.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 887: from 127 to 183
  
- Alignment No. 7010
- gi No. 2281629
- % Identity 99.6
- Alignment Length 246
- Location of Alignment in SEQ ID NO 887: from 134 to 379
  
- Alignment No. 7011
- gi No. 2281633
- % Identity 70.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 887: from 128 to 184
  
- Alignment No. 7012
- gi No. 2529675
- % Identity 100
- Alignment Length 11
- Location of Alignment in SEQ ID NO 887: from 1 to 11
  
- Alignment No. 7013
- gi No. 4587373
- % Identity 72.4
- Alignment Length 58
- Location of Alignment in SEQ ID NO 887: from 127 to 184
  
- Alignment No. 7014
- gi No. 4699734
- % Identity 72.4
- Alignment Length 58
- Location of Alignment in SEQ ID NO 887: from 128 to 184

Maximum Length Sequence corresponding to clone ID 158273

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 888
- Ceres seq\_id 1499141

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 889
- Ceres seq\_id 1499142
- Location of start within SEQ ID NO 888: at 188 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 7015
- Ribosomal protein L7/L12 C-terminal domain
- Location within SEQ ID NO 889: from 119 to 187 aa.

(D) Related Amino Acid Sequences

- Alignment No. 7016



- gi No. 223560
- % Identity 73.8
- Alignment Length 130
- Location of Alignment in SEQ ID NO 889: from 55 to 184
  
- Alignment No. 7017
- gi No. 548653
- % Identity 88.5
- Alignment Length 191
- Location of Alignment in SEQ ID NO 889: from 1 to 187
  
- Alignment No. 7018
- gi No. 548654
- % Identity 71.9
- Alignment Length 192
- Location of Alignment in SEQ ID NO 889: from 1 to 186
  
- Alignment No. 7019
- gi No. 548655
- % Identity 98.9
- Alignment Length 187
- Location of Alignment in SEQ ID NO 889: from 1 to 187

Maximum Length Sequence corresponding to clone ID 158343

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 890
- Ceres seq\_id 1499147

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 891
- Ceres seq\_id 1499148
- Location of start within SEQ ID NO 890: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 7020
- gi No. 4836917
- % Identity 82.8
- Alignment Length 209
- Location of Alignment in SEQ ID NO 891: from 1 to 208

- Alignment No. 7021
- gi No. 4836925
- % Identity 93.3
- Alignment Length 209
- Location of Alignment in SEQ ID NO 891: from 1 to 208

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 892
- Ceres seq\_id 1499149
- Location of start within SEQ ID NO 890: at 12 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 7022
- gi No. 4836917
- % Identity 82.8
- Alignment Length 209
- Location of Alignment in SEQ ID NO 892: from 1 to 205

- Alignment No. 7023
- gi No. 4836925
- % Identity 93.3
- Alignment Length 209
- Location of Alignment in SEQ ID NO 892: from 1 to 205

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 893
- Ceres seq\_id 1499150
- Location of start within SEQ ID NO 890: at 183 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 7024
- gi No. 4836917
- % Identity 82.8
- Alignment Length 209
- Location of Alignment in SEQ ID NO 893: from 1 to 148
- Alignment No. 7025
- gi No. 4836925
- % Identity 93.3
- Alignment Length 209
- Location of Alignment in SEQ ID NO 893: from 1 to 148

Maximum Length Sequence corresponding to clone ID 158418

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 894
- Ceres seq\_id 1499159

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 895
- Ceres seq\_id 1499160
- Location of start within SEQ ID NO 894: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 896
- Ceres seq\_id 1499161
- Location of start within SEQ ID NO 894: at 775 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 897
- Ceres seq\_id 1499162
- Location of start within SEQ ID NO 894: at 1212 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 7026
- gi No. 5541705
- % Identity 75.9
- Alignment Length 83
- Location of Alignment in SEQ ID NO 897: from 27 to 109

Maximum Length Sequence corresponding to clone ID 158453

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 898
- Ceres seq\_id 1499163

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 899
- Ceres seq\_id 1499164
- Location of start within SEQ ID NO 898: at 173 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 900
- Ceres seq\_id 1499165
- Location of start within SEQ ID NO 898: at 197 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 901
- Ceres seq\_id 1499166
- Location of start within SEQ ID NO 898: at 845 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 7027
- gi No. 2982259
- % Identity 71.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 901: from 1 to 115
- Alignment No. 7028
- gi No. 3914535
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 901: from 1 to 115
- Alignment No. 7029
- gi No. 4753651
- % Identity 89.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 901: from 1 to 115

Maximum Length Sequence corresponding to clone ID 158702

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 902
- Ceres seq\_id 1499185

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 903
- Ceres seq\_id 1499186
- Location of start within SEQ ID NO 902: at 103 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 7030

- Inositol monophosphatase family
- Location within SEQ ID NO 903: from 148 to 211 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 158765

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 904
- Ceres seq\_id 1499190

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 905
- Ceres seq\_id 1499191
- Location of start within SEQ ID NO 904: at 428 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 7031
- gi No. 4836922
- % Identity 94.6
- Alignment Length 37
- Location of Alignment in SEQ ID NO 905: from 1 to 37
- Alignment No. 7032
- gi No. 4836922
- % Identity 84.5
- Alignment Length 97
- Location of Alignment in SEQ ID NO 905: from 60 to 149

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 906
- Ceres seq\_id 1499192
- Location of start within SEQ ID NO 904: at 452 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 7033
- gi No. 4836922
- % Identity 94.6
- Alignment Length 37
- Location of Alignment in SEQ ID NO 906: from 1 to 29
- Alignment No. 7034
- gi No. 4836922
- % Identity 84.5
- Alignment Length 97
- Location of Alignment in SEQ ID NO 906: from 52 to 141

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 907
- Ceres seq\_id 1499193
- Location of start within SEQ ID NO 904: at 455 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 7035
- gi No. 4836922
- % Identity 94.6
- Alignment Length 37

- Maximum Length Sequence corresponding to clone ID 158882

```
- Pat. Appln. SEQ ID NO 908
- Ceres seq_id 1499194
```

- Pat. Appln. SEQ ID NO 909
- Ceres seq\_id 1499195
- Location of start within SEQ ID NO 908: at 641 nt.

- Alignment No. 7037
- Chalcone and stilbene synthases
- Location within SEQ ID NO 909: from 245 to 287 aa.

- Alignment No. 7038
- gi No. 1255207
- % Identity 71.9
- Alignment Length 349
- Location of Alignment in SEQ ID NO 909: from 1 to 345
  
- Alignment No. 7039
- gi No. 2271465
- % Identity 72.2
- Alignment Length 349
- Location of Alignment in SEQ ID NO 909: from 1 to 345
  
- Alignment No. 7040
- gi No. 2760830
- % Identity 70.3
- Alignment Length 350
- Location of Alignment in SEQ ID NO 909: from 1 to 343
  
- Alignment No. 7041
- gi No. 3075394
- % Identity 70.9
- Alignment Length 117
- Location of Alignment in SEQ ID NO 909: from 230 to 345
  
- Alignment No. 7042
- gi No. 3096920
- % Identity 80.5
- Alignment Length 353
- Location of Alignment in SEQ ID NO 909: from 1 to 345
  
- Alignment No. 7043
- gi No. 3142289
- % Identity 70.9
- Alignment Length 358
- Location of Alignment in SEQ ID NO 909: from 1 to 343
  
- Alignment No. 7044

- gi No. 3283059
- % Identity 72.6
- Alignment Length 168
- Location of Alignment in SEQ ID NO 909: from 166 to 332
  
- Alignment No. 7045
- gi No. 3283061
- % Identity 72
- Alignment Length 168
- Location of Alignment in SEQ ID NO 909: from 166 to 332
  
- Alignment No. 7046
- gi No. 3283063
- % Identity 72
- Alignment Length 168
- Location of Alignment in SEQ ID NO 909: from 166 to 332
  
- Alignment No. 7047
- gi No. 3283065
- % Identity 70.8
- Alignment Length 168
- Location of Alignment in SEQ ID NO 909: from 166 to 332
  
- Alignment No. 7048
- gi No. 4115364
- % Identity 70.5
- Alignment Length 352
- Location of Alignment in SEQ ID NO 909: from 1 to 345
  
- Alignment No. 7049
- gi No. 4544399
- % Identity 83.6
- Alignment Length 354
- Location of Alignment in SEQ ID NO 909: from 1 to 347
  
- Alignment No. 7050
- gi No. 881615
- % Identity 71.1
- Alignment Length 353
- Location of Alignment in SEQ ID NO 909: from 1 to 345

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 910
- Ceres seq\_id 1499196
- Location of start within SEQ ID NO 908: at 668 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 7051
- Chalcone and stilbene synthases
- Location within SEQ ID NO 910: from 236 to 278 aa.

(D) Related Amino Acid Sequences

- Alignment No. 7052
- gi No. 1255207
- % Identity 71.9
- Alignment Length 349
- Location of Alignment in SEQ ID NO 910: from 1 to 336
  
- Alignment No. 7053
- gi No. 2271465

- % Identity 72.2
- Alignment Length 349
- Location of Alignment in SEQ ID NO 910: from 1 to 336
  
- Alignment No. 7054
- gi No. 2760830
- % Identity 70.3
- Alignment Length 350
- Location of Alignment in SEQ ID NO 910: from 1 to 334
  
- Alignment No. 7055
- gi No. 3075394
- % Identity 70.9
- Alignment Length 117
- Location of Alignment in SEQ ID NO 910: from 221 to 336
  
- Alignment No. 7056
- gi No. 3096920
- % Identity 80.5
- Alignment Length 353
- Location of Alignment in SEQ ID NO 910: from 1 to 336
  
- Alignment No. 7057
- gi No. 3142289
- % Identity 70.9
- Alignment Length 358
- Location of Alignment in SEQ ID NO 910: from 1 to 334
  
- Alignment No. 7058
- gi No. 3283059
- % Identity 72.6
- Alignment Length 168
- Location of Alignment in SEQ ID NO 910: from 157 to 323
  
- Alignment No. 7059
- gi No. 3283061
- % Identity 72
- Alignment Length 168
- Location of Alignment in SEQ ID NO 910: from 157 to 323
  
- Alignment No. 7060
- gi No. 3283063
- % Identity 72
- Alignment Length 168
- Location of Alignment in SEQ ID NO 910: from 157 to 323
  
- Alignment No. 7061
- gi No. 3283065
- % Identity 70.8
- Alignment Length 168
- Location of Alignment in SEQ ID NO 910: from 157 to 323
  
- Alignment No. 7062
- gi No. 4115364
- % Identity 70.5
- Alignment Length 352
- Location of Alignment in SEQ ID NO 910: from 1 to 336
  
- Alignment No. 7063
- gi No. 4544399
- % Identity 83.6

- Alignment Length 354
- Location of Alignment in SEQ ID NO 910: from 1 to 338
- Alignment No. 7064
- gi No. 881615
- % Identity 71.1
- Alignment Length 353
- Location of Alignment in SEQ ID NO 910: from 1 to 336

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 911
- Ceres seq id 1499197
- Location of start within SEQ ID NO 908: at 701 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 7065
- Chalcone and stilbene synthases
- Location within SEQ ID NO 911: from 225 to 267 aa.

(D) Related Amino Acid Sequences

- Alignment No. 7066
- gi No. 1255207
- % Identity 71.9
- Alignment Length 349
- Location of Alignment in SEQ ID NO 911: from 1 to 325
- Alignment No. 7067
- gi No. 2271465
- % Identity 72.2
- Alignment Length 349
- Location of Alignment in SEQ ID NO 911: from 1 to 325
- Alignment No. 7068
- gi No. 2760830
- % Identity 70.3
- Alignment Length 350
- Location of Alignment in SEQ ID NO 911: from 1 to 323
- Alignment No. 7069
- gi No. 3075394
- % Identity 70.9
- Alignment Length 117
- Location of Alignment in SEQ ID NO 911: from 210 to 325
- Alignment No. 7070
- gi No. 3096920
- % Identity 80.5
- Alignment Length 353
- Location of Alignment in SEQ ID NO 911: from 1 to 325
- Alignment No. 7071
- gi No. 3142289
- % Identity 70.9
- Alignment Length 358
- Location of Alignment in SEQ ID NO 911: from 1 to 323
- Alignment No. 7072
- gi No. 3283059
- % Identity 72.6
- Alignment Length 168

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- Location of Alignment in SEQ ID NO 911: from 146 to 312
- Alignment No. 7073
- gi No. 3283061
- % Identity 72
- Alignment Length 168
- Location of Alignment in SEQ ID NO 911: from 146 to 312
- Alignment No. 7074
- gi No. 3283063
- % Identity 72
- Alignment Length 168
- Location of Alignment in SEQ ID NO 911: from 146 to 312
- Alignment No. 7075
- gi No. 3283065
- % Identity 70.8
- Alignment Length 168
- Location of Alignment in SEQ ID NO 911: from 146 to 312
- Alignment No. 7076
- gi No. 4115364
- % Identity 70.5
- Alignment Length 352
- Location of Alignment in SEQ ID NO 911: from 1 to 325
- Alignment No. 7077
- gi No. 4544399
- % Identity 83.6
- Alignment Length 354
- Location of Alignment in SEQ ID NO 911: from 1 to 327
- Alignment No. 7078
- gi No. 881615
- % Identity 71.1
- Alignment Length 353
- Location of Alignment in SEQ ID NO 911: from 1 to 325

Maximum Length Sequence corresponding to clone ID 159337

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 912
- Ceres seq\_id 1499198

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 913
- Ceres seq\_id 1499199
- Location of start within SEQ ID NO 912: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 7079
- Kelch motif
- Location within SEQ ID NO 913: from 23 to 69 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 914
- Ceres seq\_id 1499200
- Location of start within SEQ ID NO 912: at 71 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 7080
- Kelch motif
- Location within SEQ ID NO 914: from 1 to 46 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 915
- Ceres seq\_id 1499201
- Location of start within SEQ ID NO 912: at 116 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 159432

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 916
- Ceres seq\_id 1499206

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 917
- Ceres seq\_id 1499207
- Location of start within SEQ ID NO 916: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 7081
- Ribosomal protein S5
- Location within SEQ ID NO 917: from 100 to 237 aa.

(D) Related Amino Acid Sequences

- Alignment No. 7082
- gi No. 105987
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 917: from 15 to 46
- Alignment No. 7083
- gi No. 1173239
- % Identity 77.2
- Alignment Length 202
- Location of Alignment in SEQ ID NO 917: from 55 to 256
- Alignment No. 7084
- gi No. 126465
- % Identity 71.4
- Alignment Length 36
- Location of Alignment in SEQ ID NO 917: from 12 to 46
- Alignment No. 7085
- gi No. 133914
- % Identity 74.5
- Alignment Length 255
- Location of Alignment in SEQ ID NO 917: from 13 to 267
- Alignment No. 7086
- gi No. 1710756
- % Identity 74.8
- Alignment Length 255

- Location of Alignment in SEQ ID NO 917: from 15 to 267
- Alignment No. 7087
- gi No. 1710758
- % Identity 74.1
- Alignment Length 255
- Location of Alignment in SEQ ID NO 917: from 13 to 267
- Alignment No. 7088
- gi No. 2137785
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 917: from 21 to 47
- Alignment No. 7089
- gi No. 2137785
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 917: from 21 to 47
- Alignment No. 7090
- gi No. 2137785
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 917: from 21 to 47
- Alignment No. 7091
- gi No. 2920825
- % Identity 75.3
- Alignment Length 231
- Location of Alignment in SEQ ID NO 917: from 37 to 267
- Alignment No. 7092
- gi No. 2920827
- % Identity 72.7
- Alignment Length 245
- Location of Alignment in SEQ ID NO 917: from 23 to 267
- Alignment No. 7093
- gi No. 2920831
- % Identity 74
- Alignment Length 235
- Location of Alignment in SEQ ID NO 917: from 33 to 267
- Alignment No. 7094
- gi No. 2920833
- % Identity 75.2
- Alignment Length 226
- Location of Alignment in SEQ ID NO 917: from 42 to 267
- Alignment No. 7095
- gi No. 3122811
- % Identity 73.7
- Alignment Length 255
- Location of Alignment in SEQ ID NO 917: from 13 to 267
- Alignment No. 7096
- gi No. 3329635
- % Identity 71.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 917: from 15 to 49

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- Alignment No. 7097
- gi No. 3399667
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 917: from 15 to 46
- Alignment No. 7098
- gi No. 3642671
- % Identity 77.7
- Alignment Length 179
- Location of Alignment in SEQ ID NO 917: from 87 to 265
- Alignment No. 7099
- gi No. 3915847
- % Identity 87.2
- Alignment Length 283
- Location of Alignment in SEQ ID NO 917: from 5 to 285
- Alignment No. 7100
- gi No. 4321126
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 917: from 15 to 46
- Alignment No. 7101
- gi No. 4503661
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 917: from 15 to 46
- Alignment No. 7102
- gi No. 4506719
- % Identity 77
- Alignment Length 200
- Location of Alignment in SEQ ID NO 917: from 68 to 267
- Alignment No. 7103
- gi No. 544283
- % Identity 71
- Alignment Length 32
- Location of Alignment in SEQ ID NO 917: from 17 to 47
- Alignment No. 7104
- gi No. 91275
- % Identity 76.5
- Alignment Length 200
- Location of Alignment in SEQ ID NO 917: from 68 to 267
- Alignment No. 7105
- gi No. 929566
- % Identity 71.4
- Alignment Length 36
- Location of Alignment in SEQ ID NO 917: from 14 to 48

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 918
- Ceres seq\_id 1499208
- Location of start within SEQ ID NO 916: at 303 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 7106
- Ribosomal protein S5
- Location within SEQ ID NO 918: from 1 to 137 aa.

(D) Related Amino Acid Sequences

- Alignment No. 7107
- gi No. 1173239
- % Identity 77.2
- Alignment Length 202
- Location of Alignment in SEQ ID NO 918: from 1 to 156
- Alignment No. 7108
- gi No. 133914
- % Identity 74.5
- Alignment Length 255
- Location of Alignment in SEQ ID NO 918: from 1 to 167
- Alignment No. 7109
- gi No. 1710756
- % Identity 74.8
- Alignment Length 255
- Location of Alignment in SEQ ID NO 918: from 1 to 167
- Alignment No. 7110
- gi No. 1710758
- % Identity 74.1
- Alignment Length 255
- Location of Alignment in SEQ ID NO 918: from 1 to 167
- Alignment No. 7111
- gi No. 2920825
- % Identity 75.3
- Alignment Length 231
- Location of Alignment in SEQ ID NO 918: from 1 to 167
- Alignment No. 7112
- gi No. 2920827
- % Identity 72.7
- Alignment Length 245
- Location of Alignment in SEQ ID NO 918: from 1 to 167
- Alignment No. 7113
- gi No. 2920831
- % Identity 74
- Alignment Length 235
- Location of Alignment in SEQ ID NO 918: from 1 to 167
- Alignment No. 7114
- gi No. 2920833
- % Identity 75.2
- Alignment Length 226
- Location of Alignment in SEQ ID NO 918: from 1 to 167
- Alignment No. 7115
- gi No. 3122811
- % Identity 73.7
- Alignment Length 255
- Location of Alignment in SEQ ID NO 918: from 1 to 167

- Alignment No. 7116
- gi No. 3642671
- % Identity 77.7
- Alignment Length 179
- Location of Alignment in SEQ ID NO 918: from 1 to 165
  
- Alignment No. 7117
- gi No. 3915847
- % Identity 87.2
- Alignment Length 283
- Location of Alignment in SEQ ID NO 918: from 1 to 185
  
- Alignment No. 7118
- gi No. 4506719
- % Identity 77
- Alignment Length 200
- Location of Alignment in SEQ ID NO 918: from 1 to 167
  
- Alignment No. 7119
- gi No. 91275
- % Identity 76.5
- Alignment Length 200
- Location of Alignment in SEQ ID NO 918: from 1 to 167

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 919
- Ceres seq\_id 1499209
- Location of start within SEQ ID NO 916: at 312 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 7120
- Ribosomal protein S5
- Location within SEQ ID NO 919: from 1 to 134 aa.

(D) Related Amino Acid Sequences

- Alignment No. 7121
- gi No. 1173239
- % Identity 77.2
- Alignment Length 202
- Location of Alignment in SEQ ID NO 919: from 1 to 153
  
- Alignment No. 7122
- gi No. 133914
- % Identity 74.5
- Alignment Length 255
- Location of Alignment in SEQ ID NO 919: from 1 to 164
  
- Alignment No. 7123
- gi No. 1710756
- % Identity 74.8
- Alignment Length 255
- Location of Alignment in SEQ ID NO 919: from 1 to 164
  
- Alignment No. 7124
- gi No. 1710758
- % Identity 74.1
- Alignment Length 255
- Location of Alignment in SEQ ID NO 919: from 1 to 164
  
- Alignment No. 7125

- gi No. 2920825
- % Identity 75.3
- Alignment Length 231
- Location of Alignment in SEQ ID NO 919: from 1 to 164
  
- Alignment No. 7126
- gi No. 2920827
- % Identity 72.7
- Alignment Length 245
- Location of Alignment in SEQ ID NO 919: from 1 to 164
  
- Alignment No. 7127
- gi No. 2920831
- % Identity 74
- Alignment Length 235
- Location of Alignment in SEQ ID NO 919: from 1 to 164
  
- Alignment No. 7128
- gi No. 2920833
- % Identity 75.2
- Alignment Length 226
- Location of Alignment in SEQ ID NO 919: from 1 to 164
  
- Alignment No. 7129
- gi No. 3122811
- % Identity 73.7
- Alignment Length 255
- Location of Alignment in SEQ ID NO 919: from 1 to 164
  
- Alignment No. 7130
- gi No. 3642671
- % Identity 77.7
- Alignment Length 179
- Location of Alignment in SEQ ID NO 919: from 1 to 162
  
- Alignment No. 7131
- gi No. 3915847
- % Identity 87.2
- Alignment Length 283
- Location of Alignment in SEQ ID NO 919: from 1 to 182
  
- Alignment No. 7132
- gi No. 4506719
- % Identity 77
- Alignment Length 200
- Location of Alignment in SEQ ID NO 919: from 1 to 164
  
- Alignment No. 7133
- gi No. 91275
- % Identity 76.5
- Alignment Length 200
- Location of Alignment in SEQ ID NO 919: from 1 to 164

Maximum Length Sequence corresponding to clone ID 159437

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 920
- Ceres seq\_id 1499210

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 921
- Ceres seq\_id 1499211
- Location of start within SEQ ID NO 920: at 104 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 7134
- Actin
- Location within SEQ ID NO 921: from 38 to 130 aa.

(D) Related Amino Acid Sequences

- Alignment No. 7135
- gi No. 100990
- % Identity 82.1
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
- Alignment No. 7136
- gi No. 100990
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7137
- gi No. 10199
- % Identity 89.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 921: from 38 to 129
- Alignment No. 7138
- gi No. 1022821
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 921: from 5 to 39
- Alignment No. 7139
- gi No. 1022821
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 921: from 16 to 130
- Alignment No. 7140
- gi No. 102330
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 921: from 5 to 39
- Alignment No. 7141
- gi No. 104518
- % Identity 79.5
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
- Alignment No. 7142
- gi No. 1070613
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7143
- gi No. 1085616
- % Identity 83.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130



- Alignment No. 7144
- gi No. 1085617
- % Identity 92.6
- Alignment Length 27
- Location of Alignment in SEQ ID NO 921: from 13 to 39
  
- Alignment No. 7145
- gi No. 1085617
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7146
- gi No. 113213
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7147
- gi No. 113214
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7148
- gi No. 113214
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7149
- gi No. 113215
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7150
- gi No. 113216
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7151
- gi No. 113217
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7152
- gi No. 113217
- % Identity 76.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7153
- gi No. 113218
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130

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- Alignment No. 7154
- gi No. 113220
- % Identity 81.6
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7155
- gi No. 113220
- % Identity 93.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7156
- gi No. 113222
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7157
- gi No. 113222
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7158
- gi No. 113223
- % Identity 82.1
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
  
- Alignment No. 7159
- gi No. 113223
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7160
- gi No. 113224
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 921: from 4 to 39
  
- Alignment No. 7161
- gi No. 113226
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7162
- gi No. 113227
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
  
- Alignment No. 7163
- gi No. 113228
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7164

- gi No. 113229
- % Identity 80.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7165
- gi No. 113230
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7166
- gi No. 113231
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7167
- gi No. 113232
- % Identity 80.8
- Alignment Length 52
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7168
- gi No. 113232
- % Identity 75.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7169
- gi No. 113233
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7170
- gi No. 113239
- % Identity 75.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 921: from 7 to 39
  
- Alignment No. 7171
- gi No. 113240
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7172
- gi No. 113240
- % Identity 72.1
- Alignment Length 129
- Location of Alignment in SEQ ID NO 921: from 2 to 130
  
- Alignment No. 7173
- gi No. 113241
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 921: from 5 to 38
  
- Alignment No. 7174
- gi No. 113241

- % Identity 70.5
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7175
- gi No. 113242
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 921: from 5 to 39
  
- Alignment No. 7176
- gi No. 113242
- % Identity 71.6
- Alignment Length 95
- Location of Alignment in SEQ ID NO 921: from 38 to 132
  
- Alignment No. 7177
- gi No. 113243
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7178
- gi No. 113245
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7179
- gi No. 113246
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7180
- gi No. 113247
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7181
- gi No. 113249
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7182
- gi No. 113250
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7183
- gi No. 113250
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7184
- gi No. 113253
- % Identity 88.2

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- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7185
- gi No. 113254
- % Identity 75.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7186
- gi No. 113255
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7187
- gi No. 113256
- % Identity 76.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7188
- gi No. 113257
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7189
- gi No. 113258
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7190
- gi No. 113260
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 921: from 1 to 17
  
- Alignment No. 7191
- gi No. 113261
- % Identity 74
- Alignment Length 51
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7192
- gi No. 113261
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7193
- gi No. 113263
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7194
- gi No. 113268
- % Identity 89.2
- Alignment Length 93

- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7195
- gi No. 113271
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7196
- gi No. 113273
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7197
- gi No. 113275
- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 921: from 5 to 39
- Alignment No. 7198
- gi No. 113275
- % Identity 84.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7199
- gi No. 113276
- % Identity 79.3
- Alignment Length 87
- Location of Alignment in SEQ ID NO 921: from 38 to 124
- Alignment No. 7200
- gi No. 113277
- % Identity 71.4
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7201
- gi No. 113280
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7202
- gi No. 113281
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7203
- gi No. 113282
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7204
- gi No. 113283
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130

- Alignment No. 7205
- gi No. 113284
- % Identity 76.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7206
- gi No. 113289
- % Identity 82.1
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
  
- Alignment No. 7207
- gi No. 113289
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7208
- gi No. 113290
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7209
- gi No. 113291
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7210
- gi No. 113293
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 921: from 5 to 39
  
- Alignment No. 7211
- gi No. 113293
- % Identity 71.4
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7212
- gi No. 113294
- % Identity 73.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 921: from 21 to 130
  
- Alignment No. 7213
- gi No. 113296
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7214
- gi No. 113297
- % Identity 70.5
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130

- Alignment No. 7215
- gi No. 113298
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 921: from 6 to 43
  
- Alignment No. 7216
- gi No. 113300
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 921: from 5 to 38
  
- Alignment No. 7217
- gi No. 113300
- % Identity 70.5
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7218
- gi No. 113301
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7219
- gi No. 113302
- % Identity 91.7
- Alignment Length 24
- Location of Alignment in SEQ ID NO 921: from 107 to 130
  
- Alignment No. 7220
- gi No. 113303
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7221
- gi No. 113304
- % Identity 79.1
- Alignment Length 110
- Location of Alignment in SEQ ID NO 921: from 21 to 130
  
- Alignment No. 7222
- gi No. 113305
- % Identity 74.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7223
- gi No. 113306
- % Identity 73.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7224
- gi No. 113307
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7225



- gi No. 113308
- % Identity 76.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7226
- gi No. 113309
- % Identity 71.4
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7227
- gi No. 1168316
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7228
- gi No. 1168317
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 921: from 5 to 39
- Alignment No. 7229
- gi No. 1168317
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 921: from 16 to 130
- Alignment No. 7230
- gi No. 1168318
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7231
- gi No. 1168319
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
- Alignment No. 7232
- gi No. 1168319
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7233
- gi No. 1168320
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7234
- gi No. 1168321
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7235
- gi No. 1168322

- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 921: from 1 to 55
  
- Alignment No. 7236
- gi No. 1168322
- % Identity 86
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7237
- gi No. 1168323
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7238
- gi No. 1168324
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7239
- gi No. 1168324
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7240
- gi No. 1168325
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7241
- gi No. 1168326
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7242
- gi No. 1168337
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
  
- Alignment No. 7243
- gi No. 1168338
- % Identity 77.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7244
- gi No. 1176465
- % Identity 91.8
- Alignment Length 73
- Location of Alignment in SEQ ID NO 921: from 38 to 110
  
- Alignment No. 7245
- gi No. 1213444
- % Identity 74.1

- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7246
- gi No. 1222669
- % Identity 93.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 921: from 38 to 98
  
- Alignment No. 7247
- gi No. 1304269
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7248
- gi No. 1351866
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7249
- gi No. 1351867
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7250
- gi No. 1351868
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7251
- gi No. 1351869
- % Identity 82.8
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7252
- gi No. 1421806
- % Identity 80.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7253
- gi No. 1470107
- % Identity 93.8
- Alignment Length 32
- Location of Alignment in SEQ ID NO 921: from 38 to 69
  
- Alignment No. 7254
- gi No. 1480822
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 921: from 13 to 39
  
- Alignment No. 7255
- gi No. 1480824
- % Identity 75.9
- Alignment Length 29

- Location of Alignment in SEQ ID NO 921: from 11 to 39
- Alignment No. 7256
- gi No. 1480826
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 921: from 13 to 39
- Alignment No. 7257
- gi No. 1498326
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
- Alignment No. 7258
- gi No. 1498326
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7259
- gi No. 1498328
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
- Alignment No. 7260
- gi No. 1498328
- % Identity 92.4
- Alignment Length 92
- Location of Alignment in SEQ ID NO 921: from 39 to 130
- Alignment No. 7261
- gi No. 1498330
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
- Alignment No. 7262
- gi No. 1498330
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7263
- gi No. 1498332
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
- Alignment No. 7264
- gi No. 1498332
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7265
- gi No. 1498334
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48

- Alignment No. 7266
- gi No. 1498334
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7267
- gi No. 1498336
- % Identity 96.6
- Alignment Length 29
- Location of Alignment in SEQ ID NO 921: from 38 to 66
  
- Alignment No. 7268
- gi No. 1498336
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7269
- gi No. 1498338
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7270
- gi No. 1498338
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7271
- gi No. 1498340
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7272
- gi No. 1498340
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7273
- gi No. 1498342
- % Identity 86.4
- Alignment Length 88
- Location of Alignment in SEQ ID NO 921: from 43 to 130
  
- Alignment No. 7274
- gi No. 1498344
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7275
- gi No. 1498344
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130

- Alignment No. 7276
- gi No. 1498346
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
- Alignment No. 7277
- gi No. 1498346
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7278
- gi No. 1498382
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
- Alignment No. 7279
- gi No. 1498382
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7280
- gi No. 1498384
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
- Alignment No. 7281
- gi No. 1498384
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7282
- gi No. 1498386
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
- Alignment No. 7283
- gi No. 1498386
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7284
- gi No. 1498388
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
- Alignment No. 7285
- gi No. 1498388
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7286

- gi No. 1498390
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7287
- gi No. 1498390
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7288
- gi No. 1498393
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7289
- gi No. 1498393
- % Identity 87.2
- Alignment Length 94
- Location of Alignment in SEQ ID NO 921: from 37 to 130
  
- Alignment No. 7290
- gi No. 1498395
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7291
- gi No. 1498395
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7292
- gi No. 1519401
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7293
- gi No. 1519403
- % Identity 82.8
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7294
- gi No. 1519405
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7295
- gi No. 1531672
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7296
- gi No. 1531672

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- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7297
- gi No. 1531674
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7298
- gi No. 1531674
- % Identity 93.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7299
- gi No. 156765
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7300
- gi No. 158914
- % Identity 73.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 921: from 21 to 130
  
- Alignment No. 7301
- gi No. 161424
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7302
- gi No. 161430
- % Identity 88
- Alignment Length 92
- Location of Alignment in SEQ ID NO 921: from 38 to 129
  
- Alignment No. 7303
- gi No. 162606
- % Identity 91.5
- Alignment Length 82
- Location of Alignment in SEQ ID NO 921: from 38 to 119
  
- Alignment No. 7304
- gi No. 1666228
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7305
- gi No. 1666228
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7306
- gi No. 1666232
- % Identity 92.5



- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7307
- gi No. 1666234
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7308
- gi No. 1666234
- % Identity 88.5
- Alignment Length 96
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7309
- gi No. 1669387
- % Identity 87.2
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
  
- Alignment No. 7310
- gi No. 1669387
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7311
- gi No. 1669389
- % Identity 89.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
  
- Alignment No. 7312
- gi No. 1669389
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7313
- gi No. 168404
- % Identity 81.6
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7314
- gi No. 168404
- % Identity 93.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7315
- gi No. 1703100
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7316
- gi No. 1703101
- % Identity 75.9
- Alignment Length 112

- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7317
- gi No. 1703102
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7318
- gi No. 1703103
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7319
- gi No. 1703104
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 921: from 6 to 43
- Alignment No. 7320
- gi No. 1703105
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 921: from 6 to 43
- Alignment No. 7321
- gi No. 1703106
- % Identity 76.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7322
- gi No. 1703107
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
- Alignment No. 7323
- gi No. 1703107
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7324
- gi No. 1703108
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
- Alignment No. 7325
- gi No. 1703108
- % Identity 86.6
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7326
- gi No. 1703109
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130

- Alignment No. 7327
- gi No. 1703110
- % Identity 79.1
- Alignment Length 110
- Location of Alignment in SEQ ID NO 921: from 21 to 130
  
- Alignment No. 7328
- gi No. 1703111
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7329
- gi No. 1703112
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7330
- gi No. 1703113
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 921: from 6 to 43
  
- Alignment No. 7331
- gi No. 1703114
- % Identity 80
- Alignment Length 110
- Location of Alignment in SEQ ID NO 921: from 21 to 130
  
- Alignment No. 7332
- gi No. 1703115
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7333
- gi No. 1703115
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7334
- gi No. 1703116
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7335
- gi No. 1703117
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7336
- gi No. 1703118
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130

- Alignment No. 7337
- gi No. 1703119
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7338
- gi No. 1703119
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7339
- gi No. 1703120
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7340
- gi No. 1703121
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7341
- gi No. 1703122
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7342
- gi No. 1703123
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7343
- gi No. 1703124
- % Identity 82.9
- Alignment Length 35
- Location of Alignment in SEQ ID NO 921: from 5 to 39
  
- Alignment No. 7344
- gi No. 1703124
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7345
- gi No. 1703125
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7346
- gi No. 1703127
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7347

- gi No. 1703128
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7348
- gi No. 1703129
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7349
- gi No. 1703129
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7350
- gi No. 1703130
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7351
- gi No. 1703131
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7352
- gi No. 1703131
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7353
- gi No. 1703132
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7354
- gi No. 1703133
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7355
- gi No. 1703134
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7356
- gi No. 1703135
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7357
- gi No. 1703136

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- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7358
- gi No. 1703137
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7359
- gi No. 1703138
- % Identity 71.4
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7360
- gi No. 1703139
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7361
- gi No. 1703140
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7362
- gi No. 1703141
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7363
- gi No. 1703142
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7364
- gi No. 1703147
- % Identity 80.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7365
- gi No. 1703148
- % Identity 77.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 921: from 19 to 119
  
- Alignment No. 7366
- gi No. 1703149
- % Identity 79.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7367
- gi No. 1703151
- % Identity 76.8

- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7368
- gi No. 1703152
- % Identity 71.3
- Alignment Length 94
- Location of Alignment in SEQ ID NO 921: from 38 to 131
  
- Alignment No. 7369
- gi No. 1703153
- % Identity 85.7
- Alignment Length 35
- Location of Alignment in SEQ ID NO 921: from 5 to 39
  
- Alignment No. 7370
- gi No. 1703154
- % Identity 82.1
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
  
- Alignment No. 7371
- gi No. 1703154
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7372
- gi No. 1703155
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 921: from 5 to 39
  
- Alignment No. 7373
- gi No. 1703156
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7374
- gi No. 1703157
- % Identity 83.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7375
- gi No. 1703158
- % Identity 83.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7376
- gi No. 1703159
- % Identity 100
- Alignment Length 28
- Location of Alignment in SEQ ID NO 921: from 38 to 65
  
- Alignment No. 7377
- gi No. 1703160
- % Identity 76.9
- Alignment Length 39

- Location of Alignment in SEQ ID NO 921: from 1 to 39
- Alignment No. 7378
- gi No. 178067
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7379
- gi No. 1813478
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
- Alignment No. 7380
- gi No. 1871174
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 921: from 1 to 39
- Alignment No. 7381
- gi No. 1871174
- % Identity 71.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 921: from 23 to 130
- Alignment No. 7382
- gi No. 1871175
- % Identity 73.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7383
- gi No. 1906607
- % Identity 75.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7384
- gi No. 1944203
- % Identity 80.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 921: from 19 to 119
- Alignment No. 7385
- gi No. 20322
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
- Alignment No. 7386
- gi No. 20322
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7387
- gi No. 2072156
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130



- Alignment No. 7388
- gi No. 2119321
- % Identity 80.9
- Alignment Length 47
- Location of Alignment in SEQ ID NO 921: from 84 to 130
  
- Alignment No. 7389
- gi No. 2119326
- % Identity 81.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 921: from 5 to 37
  
- Alignment No. 7390
- gi No. 2129524
- % Identity 94.1
- Alignment Length 34
- Location of Alignment in SEQ ID NO 921: from 6 to 39
  
- Alignment No. 7391
- gi No. 2129524
- % Identity 86.3
- Alignment Length 95
- Location of Alignment in SEQ ID NO 921: from 38 to 132
  
- Alignment No. 7392
- gi No. 2129529
- % Identity 89.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
  
- Alignment No. 7393
- gi No. 2129529
- % Identity 86.3
- Alignment Length 95
- Location of Alignment in SEQ ID NO 921: from 38 to 132
  
- Alignment No. 7394
- gi No. 2136927
- % Identity 77.6
- Alignment Length 49
- Location of Alignment in SEQ ID NO 921: from 82 to 130
  
- Alignment No. 7395
- gi No. 223071
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7396
- gi No. 2231555
- % Identity 71.4
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7397
- gi No. 2231557
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130

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- Alignment No. 7398
- gi No. 2231561
- % Identity 70.5
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7399
- gi No. 223390
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 921: from 6 to 43
  
- Alignment No. 7400
- gi No. 223855
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7401
- gi No. 224304
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7402
- gi No. 224305
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7403
- gi No. 224306
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7404
- gi No. 2244734
- % Identity 97.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 921: from 46 to 130
  
- Alignment No. 7405
- gi No. 225100
- % Identity 73.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7406
- gi No. 2253214
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7407
- gi No. 2253214
- % Identity 77.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7408

- gi No. 2253217
- % Identity 81.5
- Alignment Length 92
- Location of Alignment in SEQ ID NO 921: from 39 to 130
  
- Alignment No. 7409
- gi No. 2253219
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7410
- gi No. 2253219
- % Identity 73.6
- Alignment Length 129
- Location of Alignment in SEQ ID NO 921: from 2 to 130
  
- Alignment No. 7411
- gi No. 2253221
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7412
- gi No. 2253223
- % Identity 72.8
- Alignment Length 114
- Location of Alignment in SEQ ID NO 921: from 19 to 132
  
- Alignment No. 7413
- gi No. 2289966
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 921: from 97 to 130
  
- Alignment No. 7414
- gi No. 2289971
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 921: from 97 to 130
  
- Alignment No. 7415
- gi No. 2289975
- % Identity 83.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7416
- gi No. 229690
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7417
- gi No. 2304965
- % Identity 86
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7418
- gi No. 2304969

- % Identity 76.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7419
- gi No. 231494
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7420
- gi No. 231495
- % Identity 81.6
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7421
- gi No. 231495
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7422
- gi No. 231496
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7423
- gi No. 231496
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7424
- gi No. 231498
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7425
- gi No. 231499
- % Identity 81.6
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7426
- gi No. 231499
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7427
- gi No. 231501
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7428
- gi No. 231501
- % Identity 86.2

- Alignment Length 87
- Location of Alignment in SEQ ID NO 921: from 44 to 130
- Alignment No. 7429
- gi No. 231502
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
- Alignment No. 7430
- gi No. 231502
- % Identity 95.6
- Alignment Length 68
- Location of Alignment in SEQ ID NO 921: from 38 to 105
- Alignment No. 7431
- gi No. 231503
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
- Alignment No. 7432
- gi No. 231503
- % Identity 93.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7433
- gi No. 231504
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
- Alignment No. 7434
- gi No. 231504
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7435
- gi No. 231505
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
- Alignment No. 7436
- gi No. 231505
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7437
- gi No. 231506
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7438
- gi No. 2315847
- % Identity 90.3
- Alignment Length 93

- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7439
- gi No. 2315849
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7440
- gi No. 2318133
- % Identity 84.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7441
- gi No. 2318135
- % Identity 82.9
- Alignment Length 35
- Location of Alignment in SEQ ID NO 921: from 5 to 39
- Alignment No. 7442
- gi No. 2318135
- % Identity 84.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7443
- gi No. 2492664
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7444
- gi No. 2492666
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7445
- gi No. 2492668
- % Identity 82.1
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
- Alignment No. 7446
- gi No. 2492668
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7447
- gi No. 2492669
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 921: from 96 to 130
- Alignment No. 7448
- gi No. 2492670
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 921: from 106 to 130

- Alignment No. 7449
- gi No. 2492671
- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 921: from 96 to 130
  
- Alignment No. 7450
- gi No. 2492672
- % Identity 80.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7451
- gi No. 2492674
- % Identity 79.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7452
- gi No. 2588914
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7453
- gi No. 2624850
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7454
- gi No. 2641233
- % Identity 71
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7455
- gi No. 2641235
- % Identity 70.7
- Alignment Length 92
- Location of Alignment in SEQ ID NO 921: from 38 to 129
  
- Alignment No. 7456
- gi No. 2642634
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 921: from 38 to 57
  
- Alignment No. 7457
- gi No. 2665740
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7458
- gi No. 2724046
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130

- Alignment No. 7459
- gi No. 2829750
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7460
- gi No. 2829754
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7461
- gi No. 2829755
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7462
- gi No. 2833326
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7463
- gi No. 2887459
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7464
- gi No. 2944389
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7465
- gi No. 2944389
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7466
- gi No. 294852
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7467
- gi No. 2967678
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7468
- gi No. 2981073
- % Identity 89.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 921: from 56 to 130
  
- Alignment No. 7469



- gi No. 3036959
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7470
- gi No. 3044210
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7471
- gi No. 3046986
- % Identity 79.5
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
  
- Alignment No. 7472
- gi No. 3046986
- % Identity 78.7
- Alignment Length 94
- Location of Alignment in SEQ ID NO 921: from 38 to 131
  
- Alignment No. 7473
- gi No. 309090
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7474
- gi No. 3107919
- % Identity 72.3
- Alignment Length 48
- Location of Alignment in SEQ ID NO 921: from 3 to 48
  
- Alignment No. 7475
- gi No. 3107919
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7476
- gi No. 311755
- % Identity 88
- Alignment Length 92
- Location of Alignment in SEQ ID NO 921: from 38 to 129
  
- Alignment No. 7477
- gi No. 3121741
- % Identity 76.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7478
- gi No. 3121742
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7479
- gi No. 3123181

- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7480
- gi No. 3127131
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7481
- gi No. 3127133
- % Identity 72
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7482
- gi No. 3127133
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 921: from 16 to 130
  
- Alignment No. 7483
- gi No. 3127135
- % Identity 78.6
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7484
- gi No. 3127137
- % Identity 79.3
- Alignment Length 92
- Location of Alignment in SEQ ID NO 921: from 39 to 130
  
- Alignment No. 7485
- gi No. 3182886
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7486
- gi No. 3182891
- % Identity 80.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7487
- gi No. 3182892
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7488
- gi No. 3182893
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7489
- gi No. 3182894
- % Identity 87.1

- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7490
- gi No. 3182895
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7491
- gi No. 3182896
- % Identity 83.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7492
- gi No. 3182897
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7493
- gi No. 3182898
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7494
- gi No. 3182899
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7495
- gi No. 3182902
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7496
- gi No. 3182903
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7497
- gi No. 3182904
- % Identity 79.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7498
- gi No. 3182905
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7499
- gi No. 3182906
- % Identity 79.6
- Alignment Length 93

- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7500
- gi No. 3219758
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
- Alignment No. 7501
- gi No. 3219758
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7502
- gi No. 3219759
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
- Alignment No. 7503
- gi No. 3219759
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7504
- gi No. 3219760
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
- Alignment No. 7505
- gi No. 3219760
- % Identity 93.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7506
- gi No. 3219761
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
- Alignment No. 7507
- gi No. 3219761
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7508
- gi No. 3219762
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
- Alignment No. 7509
- gi No. 3219762
- % Identity 81.7
- Alignment Length 117
- Location of Alignment in SEQ ID NO 921: from 16 to 130

- Alignment No. 7510
- gi No. 3219763
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7511
- gi No. 3219763
- % Identity 76.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7512
- gi No. 3219764
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7513
- gi No. 3219764
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7514
- gi No. 3219765
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7515
- gi No. 3219765
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7516
- gi No. 3219766
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7517
- gi No. 3219766
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7518
- gi No. 3219767
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7519
- gi No. 3219767
- % Identity 84
- Alignment Length 94
- Location of Alignment in SEQ ID NO 921: from 38 to 130

- Alignment No. 7520
- gi No. 3219768
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7521
- gi No. 3219768
- % Identity 83.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7522
- gi No. 3219769
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7523
- gi No. 3219769
- % Identity 84.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7524
- gi No. 3219770
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7525
- gi No. 3219770
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7526
- gi No. 3219771
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7527
- gi No. 3219771
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7528
- gi No. 3219772
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7529
- gi No. 3219772
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7530

- gi No. 3219773
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7531
- gi No. 3219773
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7532
- gi No. 3287956
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7533
- gi No. 3287956
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7534
- gi No. 3319951
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7535
- gi No. 3328
- % Identity 72.3
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7536
- gi No. 3336984
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7537
- gi No. 3348131
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7538
- gi No. 3386376
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7539
- gi No. 3386380
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7540
- gi No. 3386382

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- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7541
- gi No. 3396073
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7542
- gi No. 3420239
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7543
- gi No. 3420239
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7544
- gi No. 3421457
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7545
- gi No. 3642631
- % Identity 85.1
- Alignment Length 47
- Location of Alignment in SEQ ID NO 921: from 84 to 130
  
- Alignment No. 7546
- gi No. 3746936
- % Identity 74
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7547
- gi No. 3746936
- % Identity 79.5
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7548
- gi No. 3746938
- % Identity 74
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7549
- gi No. 3746938
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7550
- gi No. 3746940
- % Identity 80



- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
- Alignment No. 7551
- gi No. 3746940
- % Identity 79.5
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7552
- gi No. 3746942
- % Identity 75.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 921: from 18 to 48
- Alignment No. 7553
- gi No. 3746942
- % Identity 79.5
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7554
- gi No. 3860544
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7555
- gi No. 387082
- % Identity 72.3
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7556
- gi No. 3879474
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7557
- gi No. 3880219
- % Identity 84.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7558
- gi No. 3907620
- % Identity 83.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7559
- gi No. 3907622
- % Identity 77.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7560
- gi No. 3912969
- % Identity 87.1
- Alignment Length 93

- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7561
- gi No. 3924630
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7562
- gi No. 398464
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 921: from 40 to 64
- Alignment No. 7563
- gi No. 399003
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7564
- gi No. 4009328
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7565
- gi No. 409694
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7566
- gi No. 4105262
- % Identity 87.2
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
- Alignment No. 7567
- gi No. 4105262
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7568
- gi No. 4138667
- % Identity 77.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7569
- gi No. 4139264
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
- Alignment No. 7570
- gi No. 4139264
- % Identity 86.6
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130

- Alignment No. 7571
- gi No. 4204812
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7572
- gi No. 4235277
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7573
- gi No. 4249564
- % Identity 79.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7574
- gi No. 4261646
- % Identity 75.5
- Alignment Length 94
- Location of Alignment in SEQ ID NO 921: from 19 to 112
  
- Alignment No. 7575
- gi No. 4261647
- % Identity 75.5
- Alignment Length 94
- Location of Alignment in SEQ ID NO 921: from 19 to 112
  
- Alignment No. 7576
- gi No. 4261859
- % Identity 82.9
- Alignment Length 35
- Location of Alignment in SEQ ID NO 921: from 5 to 39
  
- Alignment No. 7577
- gi No. 4376057
- % Identity 87.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 921: from 53 to 130
  
- Alignment No. 7578
- gi No. 4376177
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 921: from 52 to 130
  
- Alignment No. 7579
- gi No. 4501881
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7580
- gi No. 4501883
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130

- Alignment No. 7581
- gi No. 4501885
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7582
- gi No. 4501887
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7583
- gi No. 4501889
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7584
- gi No. 4512327
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 921: from 21 to 48
  
- Alignment No. 7585
- gi No. 4587217
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7586
- gi No. 461465
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7587
- gi No. 461465
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7588
- gi No. 467215
- % Identity 79.1
- Alignment Length 110
- Location of Alignment in SEQ ID NO 921: from 21 to 130
  
- Alignment No. 7589
- gi No. 4730817
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7590
- gi No. 476332
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7591

- gi No. 476768
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7592
- gi No. 477248
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7593
- gi No. 481515
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7594
- gi No. 4837604
- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 921: from 3 to 39
  
- Alignment No. 7595
- gi No. 4837604
- % Identity 70.9
- Alignment Length 110
- Location of Alignment in SEQ ID NO 921: from 21 to 130
  
- Alignment No. 7596
- gi No. 4837606
- % Identity 73.2
- Alignment Length 41
- Location of Alignment in SEQ ID NO 921: from 10 to 48
  
- Alignment No. 7597
- gi No. 4837608
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
  
- Alignment No. 7598
- gi No. 4837610
- % Identity 77.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7599
- gi No. 4850238
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
  
- Alignment No. 7600
- gi No. 4850238
- % Identity 76.9
- Alignment Length 108
- Location of Alignment in SEQ ID NO 921: from 23 to 130
  
- Alignment No. 7601
- gi No. 4850240

- % Identity 79.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7602
- gi No. 4885049
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7603
- gi No. 4887630
- % Identity 84.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7604
- gi No. 4902905
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7605
- gi No. 49864
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7606
- gi No. 49868
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7607
- gi No. 5031514
- % Identity 82.8
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7608
- gi No. 5031524
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 921: from 5 to 39
  
- Alignment No. 7609
- gi No. 5031524
- % Identity 76.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7610
- gi No. 5053109
- % Identity 82.8
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7611
- gi No. 5114428
- % Identity 87.1

- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7612
- gi No. 5230839
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7613
- gi No. 5230841
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7614
- gi No. 5230841
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7615
- gi No. 543484
- % Identity 77.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7616
- gi No. 543766
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 921: from 5 to 39
  
- Alignment No. 7617
- gi No. 543766
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7618
- gi No. 543767
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7619
- gi No. 543768
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7620
- gi No. 5578749
- % Identity 80.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7621
- gi No. 5597005
- % Identity 76.3
- Alignment Length 93

- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7622
- gi No. 567192
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7623
- gi No. 5679334
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7624
- gi No. 5702223
- % Identity 72.3
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7625
- gi No. 5702225
- % Identity 82.8
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7626
- gi No. 5702227
- % Identity 72.3
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7627
- gi No. 5702229
- % Identity 72.3
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7628
- gi No. 5714751
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7629
- gi No. 5726016
- % Identity 78
- Alignment Length 41
- Location of Alignment in SEQ ID NO 921: from 10 to 48
- Alignment No. 7630
- gi No. 5726016
- % Identity 70.9
- Alignment Length 117
- Location of Alignment in SEQ ID NO 921: from 19 to 135
- Alignment No. 7631
- gi No. 5726018
- % Identity 78
- Alignment Length 41
- Location of Alignment in SEQ ID NO 921: from 10 to 48



- Alignment No. 7632
- gi No. 5726018
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7633
- gi No. 5726020
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 921: from 13 to 48
- Alignment No. 7634
- gi No. 5726020
- % Identity 77.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7635
- gi No. 5751
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7636
- gi No. 576368
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7637
- gi No. 602958
- % Identity 78.6
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7638
- gi No. 627194
- % Identity 72.2
- Alignment Length 54
- Location of Alignment in SEQ ID NO 921: from 21 to 74
- Alignment No. 7639
- gi No. 627304
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7640
- gi No. 627834
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7641
- gi No. 63018
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130

- Alignment No. 7642
- gi No. 630802
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7643
- gi No. 64509
- % Identity 75.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7644
- gi No. 6628
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7645
- gi No. 683725
- % Identity 89.8
- Alignment Length 88
- Location of Alignment in SEQ ID NO 921: from 38 to 125
  
- Alignment No. 7646
- gi No. 693709
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7647
- gi No. 71611
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7648
- gi No. 71614
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7649
- gi No. 71616
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7650
- gi No. 71620
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7651
- gi No. 71621
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7652

- gi No. 71622
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7653
- gi No. 71625
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7654
- gi No. 71627
- % Identity 86
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7655
- gi No. 71629
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7656
- gi No. 71634
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7657
- gi No. 71634
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7658
- gi No. 71638
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7659
- gi No. 71638
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7660
- gi No. 71639
- % Identity 74.5
- Alignment Length 51
- Location of Alignment in SEQ ID NO 921: from 1 to 48
  
- Alignment No. 7661
- gi No. 71639
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7662
- gi No. 7183

- % Identity 70.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 921: from 3 to 48
  
- Alignment No. 7663
- gi No. 7185
- % Identity 72.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 921: from 3 to 48
  
- Alignment No. 7664
- gi No. 7187
- % Identity 73.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 921: from 6 to 39
  
- Alignment No. 7665
- gi No. 7191
- % Identity 72.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 921: from 3 to 48
  
- Alignment No. 7666
- gi No. 728791
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7667
- gi No. 728792
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7668
- gi No. 728793
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7669
- gi No. 728796
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7670
- gi No. 728798
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7671
- gi No. 797290
- % Identity 76.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
  
- Alignment No. 7672
- gi No. 809561
- % Identity 89.2

- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7673
- gi No. 83999
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
  
- Alignment No. 7674
- gi No. 84000
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 921: from 1 to 39
  
- Alignment No. 7675
- gi No. 84082
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7676
- gi No. 84344
- % Identity 73.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7677
- gi No. 84751
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7678
- gi No. 85358
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7679
- gi No. 85495
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7680
- gi No. 86169
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7681
- gi No. 86742
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
  
- Alignment No. 7682
- gi No. 871546
- % Identity 81.7
- Alignment Length 93

- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7683
- gi No. 90263
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7684
- gi No. 940010
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 921: from 38 to 130
- Alignment No. 7685
- gi No. 950002
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 921: from 19 to 130
- Alignment No. 7686
- gi No. 998468
- % Identity 100
- Alignment Length 19
- Location of Alignment in SEQ ID NO 921: from 21 to 39

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 922
- Ceres seq\_id 1499212
- Location of start within SEQ ID NO 920: at 155 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 7687
- Actin
- Location within SEQ ID NO 922: from 21 to 113 aa.

(D) Related Amino Acid Sequences

- Alignment No. 7688
- gi No. 100990
- % Identity 82.1
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
- Alignment No. 7689
- gi No. 100990
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 7690
- gi No. 10199
- % Identity 89.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 922: from 21 to 112
- Alignment No. 7691
- gi No. 1022821
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 922: from 1 to 22

- Alignment No. 7692
- gi No. 1022821
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 922: from 1 to 113
  
- Alignment No. 7693
- gi No. 102330
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 7694
- gi No. 104518
- % Identity 79.5
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 7695
- gi No. 1070613
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7696
- gi No. 1085616
- % Identity 83.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7697
- gi No. 1085617
- % Identity 92.6
- Alignment Length 27
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 7698
- gi No. 1085617
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7699
- gi No. 113213
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7700
- gi No. 113214
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7701
- gi No. 113214
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113

- Alignment No. 7702
- gi No. 113215
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7703
- gi No. 113216
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7704
- gi No. 113217
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7705
- gi No. 113217
- % Identity 76.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7706
- gi No. 113218
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7707
- gi No. 113220
- % Identity 81.6
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7708
- gi No. 113220
- % Identity 93.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7709
- gi No. 113222
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7710
- gi No. 113222
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7711
- gi No. 113223
- % Identity 82.1
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 7712



- gi No. 113223
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7713
- gi No. 113224
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 7714
- gi No. 113226
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7715
- gi No. 113227
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 7716
- gi No. 113228
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7717
- gi No. 113229
- % Identity 80.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7718
- gi No. 113230
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7719
- gi No. 113231
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7720
- gi No. 113232
- % Identity 80.8
- Alignment Length 52
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7721
- gi No. 113232
- % Identity 75.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7722
- gi No. 113233

- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7723
- gi No. 113239
- % Identity 75.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 7724
- gi No. 113240
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7725
- gi No. 113240
- % Identity 72.1
- Alignment Length 129
- Location of Alignment in SEQ ID NO 922: from 1 to 113
  
- Alignment No. 7726
- gi No. 113241
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 922: from 1 to 21
  
- Alignment No. 7727
- gi No. 113241
- % Identity 70.5
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7728
- gi No. 113242
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 7729
- gi No. 113242
- % Identity 71.6
- Alignment Length 95
- Location of Alignment in SEQ ID NO 922: from 21 to 115
  
- Alignment No. 7730
- gi No. 113243
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7731
- gi No. 113245
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7732
- gi No. 113246
- % Identity 75

- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 7733
- gi No. 113247
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7734
- gi No. 113249
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7735
- gi No. 113250
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
- Alignment No. 7736
- gi No. 113250
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7737
- gi No. 113253
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7738
- gi No. 113254
- % Identity 75.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 7739
- gi No. 113255
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7740
- gi No. 113256
- % Identity 76.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7741
- gi No. 113257
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7742
- gi No. 113258
- % Identity 89.2
- Alignment Length 93

- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7743
- gi No. 113261
- % Identity 74
- Alignment Length 51
- Location of Alignment in SEQ ID NO 922: from 1 to 31
- Alignment No. 7744
- gi No. 113261
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7745
- gi No. 113263
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7746
- gi No. 113268
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7747
- gi No. 113271
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7748
- gi No. 113273
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7749
- gi No. 113275
- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 922: from 1 to 22
- Alignment No. 7750
- gi No. 113275
- % Identity 84.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7751
- gi No. 113276
- % Identity 79.3
- Alignment Length 87
- Location of Alignment in SEQ ID NO 922: from 21 to 107
- Alignment No. 7752
- gi No. 113277
- % Identity 71.4
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113

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- Alignment No. 7753
- gi No. 113280
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 7754
- gi No. 113281
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7755
- gi No. 113282
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7756
- gi No. 113283
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 7757
- gi No. 113284
- % Identity 76.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 7758
- gi No. 113289
- % Identity 82.1
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
- Alignment No. 7759
- gi No. 113289
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 7760
- gi No. 113290
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7761
- gi No. 113291
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7762
- gi No. 113293
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 922: from 1 to 22

- Alignment No. 7763
- gi No. 113293
- % Identity 71.4
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7764
- gi No. 113294
- % Identity 73.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 922: from 4 to 113
  
- Alignment No. 7765
- gi No. 113296
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7766
- gi No. 113297
- % Identity 70.5
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7767
- gi No. 113298
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 922: from 1 to 26
  
- Alignment No. 7768
- gi No. 113300
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 922: from 1 to 21
  
- Alignment No. 7769
- gi No. 113300
- % Identity 70.5
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7770
- gi No. 113301
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7771
- gi No. 113302
- % Identity 91.7
- Alignment Length 24
- Location of Alignment in SEQ ID NO 922: from 90 to 113
  
- Alignment No. 7772
- gi No. 113303
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7773

- gi No. 113304
- % Identity 79.1
- Alignment Length 110
- Location of Alignment in SEQ ID NO 922: from 4 to 113
  
- Alignment No. 7774
- gi No. 113305
- % Identity 74.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7775
- gi No. 113306
- % Identity 73.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7776
- gi No. 113307
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7777
- gi No. 113308
- % Identity 76.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7778
- gi No. 113309
- % Identity 71.4
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7779
- gi No. 1168316
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7780
- gi No. 1168317
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 7781
- gi No. 1168317
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 922: from 1 to 113
  
- Alignment No. 7782
- gi No. 1168318
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7783
- gi No. 1168319

- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
- Alignment No. 7784
- gi No. 1168319
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7785
- gi No. 1168320
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7786
- gi No. 1168321
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7787
- gi No. 1168322
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 922: from 1 to 38
- Alignment No. 7788
- gi No. 1168322
- % Identity 86
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7789
- gi No. 1168323
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7790
- gi No. 1168324
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
- Alignment No. 7791
- gi No. 1168324
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7792
- gi No. 1168325
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7793
- gi No. 1168326
- % Identity 74.1



- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7794
- gi No. 1168337
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 7795
- gi No. 1168338
- % Identity 77.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7796
- gi No. 1176465
- % Identity 91.8
- Alignment Length 73
- Location of Alignment in SEQ ID NO 922: from 21 to 93
  
- Alignment No. 7797
- gi No. 1213444
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7798
- gi No. 1222669
- % Identity 93.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 922: from 21 to 81
  
- Alignment No. 7799
- gi No. 1304269
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7800
- gi No. 1351866
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7801
- gi No. 1351867
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7802
- gi No. 1351868
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7803
- gi No. 1351869
- % Identity 82.8
- Alignment Length 93

- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7804
- gi No. 1421806
- % Identity 80.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7805
- gi No. 1470107
- % Identity 93.8
- Alignment Length 32
- Location of Alignment in SEQ ID NO 922: from 21 to 52
- Alignment No. 7806
- gi No. 1480822
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 922: from 1 to 22
- Alignment No. 7807
- gi No. 1480824
- % Identity 75.9
- Alignment Length 29
- Location of Alignment in SEQ ID NO 922: from 1 to 22
- Alignment No. 7808
- gi No. 1480826
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 922: from 1 to 22
- Alignment No. 7809
- gi No. 1498326
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
- Alignment No. 7810
- gi No. 1498326
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 7811
- gi No. 1498328
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
- Alignment No. 7812
- gi No. 1498328
- % Identity 92.4
- Alignment Length 92
- Location of Alignment in SEQ ID NO 922: from 22 to 113
- Alignment No. 7813
- gi No. 1498330
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31

- Alignment No. 7814
- gi No. 1498330
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7815
- gi No. 1498332
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7816
- gi No. 1498332
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7817
- gi No. 1498334
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7818
- gi No. 1498334
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7819
- gi No. 1498336
- % Identity 96.6
- Alignment Length 29
- Location of Alignment in SEQ ID NO 922: from 21 to 49
  
- Alignment No. 7820
- gi No. 1498336
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7821
- gi No. 1498338
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7822
- gi No. 1498338
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7823
- gi No. 1498340
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31

- Alignment No. 7824
- gi No. 1498340
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7825
- gi No. 1498342
- % Identity 86.4
- Alignment Length 88
- Location of Alignment in SEQ ID NO 922: from 26 to 113
  
- Alignment No. 7826
- gi No. 1498344
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7827
- gi No. 1498344
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7828
- gi No. 1498346
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7829
- gi No. 1498346
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7830
- gi No. 1498382
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7831
- gi No. 1498382
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7832
- gi No. 1498384
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7833
- gi No. 1498384
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7834

- gi No. 1498386
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7835
- gi No. 1498386
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7836
- gi No. 1498388
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7837
- gi No. 1498388
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7838
- gi No. 1498390
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7839
- gi No. 1498390
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7840
- gi No. 1498393
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7841
- gi No. 1498393
- % Identity 87.2
- Alignment Length 94
- Location of Alignment in SEQ ID NO 922: from 20 to 113
  
- Alignment No. 7842
- gi No. 1498395
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7843
- gi No. 1498395
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7844
- gi No. 1519401

- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7845
- gi No. 1519403
- % Identity 82.8
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7846
- gi No. 1519405
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7847
- gi No. 1531672
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7848
- gi No. 1531672
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7849
- gi No. 1531674
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7850
- gi No. 1531674
- % Identity 93.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7851
- gi No. 156765
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7852
- gi No. 158914
- % Identity 73.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 922: from 4 to 113
  
- Alignment No. 7853
- gi No. 161424
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7854
- gi No. 161430
- % Identity 88

- Alignment Length 92
- Location of Alignment in SEQ ID NO 922: from 21 to 112
  
- Alignment No. 7855
- gi No. 162606
- % Identity 91.5
- Alignment Length 82
- Location of Alignment in SEQ ID NO 922: from 21 to 102
  
- Alignment No. 7856
- gi No. 1666228
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7857
- gi No. 1666228
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7858
- gi No. 1666232
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7859
- gi No. 1666234
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7860
- gi No. 1666234
- % Identity 88.5
- Alignment Length 96
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7861
- gi No. 1669387
- % Identity 87.2
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 7862
- gi No. 1669387
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7863
- gi No. 1669389
- % Identity 89.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 7864
- gi No. 1669389
- % Identity 89.2
- Alignment Length 93

- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7865
- gi No. 168404
- % Identity 81.6
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
- Alignment No. 7866
- gi No. 168404
- % Identity 93.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7867
- gi No. 1703100
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7868
- gi No. 1703101
- % Identity 75.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 7869
- gi No. 1703102
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7870
- gi No. 1703103
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7871
- gi No. 1703104
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 922: from 1 to 26
- Alignment No. 7872
- gi No. 1703105
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 922: from 1 to 26
- Alignment No. 7873
- gi No. 1703106
- % Identity 76.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 7874
- gi No. 1703107
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31



- Alignment No. 7875
- gi No. 1703107
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7876
- gi No. 1703108
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7877
- gi No. 1703108
- % Identity 86.6
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7878
- gi No. 1703109
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7879
- gi No. 1703110
- % Identity 79.1
- Alignment Length 110
- Location of Alignment in SEQ ID NO 922: from 4 to 113
  
- Alignment No. 7880
- gi No. 1703111
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7881
- gi No. 1703112
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7882
- gi No. 1703113
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 922: from 1 to 26
  
- Alignment No. 7883
- gi No. 1703114
- % Identity 80
- Alignment Length 110
- Location of Alignment in SEQ ID NO 922: from 4 to 113
  
- Alignment No. 7884
- gi No. 1703115
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31

- Alignment No. 7885
- gi No. 1703115
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7886
- gi No. 1703116
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7887
- gi No. 1703117
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7888
- gi No. 1703118
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7889
- gi No. 1703119
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7890
- gi No. 1703119
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7891
- gi No. 1703120
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7892
- gi No. 1703121
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7893
- gi No. 1703122
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7894
- gi No. 1703123
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7895

- gi No. 1703124
- % Identity 82.9
- Alignment Length 35
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 7896
- gi No. 1703124
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7897
- gi No. 1703125
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7898
- gi No. 1703127
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7899
- gi No. 1703128
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7900
- gi No. 1703129
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7901
- gi No. 1703129
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7902
- gi No. 1703130
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7903
- gi No. 1703131
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7904
- gi No. 1703131
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7905
- gi No. 1703132

- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7906
- gi No. 1703133
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7907
- gi No. 1703134
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7908
- gi No. 1703135
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7909
- gi No. 1703136
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7910
- gi No. 1703137
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7911
- gi No. 1703138
- % Identity 71.4
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7912
- gi No. 1703139
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7913
- gi No. 1703140
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7914
- gi No. 1703141
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7915
- gi No. 1703142
- % Identity 75

- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 7916
- gi No. 1703147
- % Identity 80.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7917
- gi No. 1703148
- % Identity 77.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 922: from 2 to 102
- Alignment No. 7918
- gi No. 1703149
- % Identity 79.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7919
- gi No. 1703151
- % Identity 76.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 7920
- gi No. 1703152
- % Identity 71.3
- Alignment Length 94
- Location of Alignment in SEQ ID NO 922: from 21 to 114
- Alignment No. 7921
- gi No. 1703153
- % Identity 85.7
- Alignment Length 35
- Location of Alignment in SEQ ID NO 922: from 1 to 22
- Alignment No. 7922
- gi No. 1703154
- % Identity 82.1
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
- Alignment No. 7923
- gi No. 1703154
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7924
- gi No. 1703155
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 922: from 1 to 22
- Alignment No. 7925
- gi No. 1703156
- % Identity 89.2
- Alignment Length 93

- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7926
- gi No. 1703157
- % Identity 83.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7927
- gi No. 1703158
- % Identity 83.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7928
- gi No. 1703159
- % Identity 100
- Alignment Length 28
- Location of Alignment in SEQ ID NO 922: from 21 to 48
- Alignment No. 7929
- gi No. 1703160
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
- Alignment No. 7930
- gi No. 178067
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 7931
- gi No. 1813478
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
- Alignment No. 7932
- gi No. 1871174
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 922: from 1 to 22
- Alignment No. 7933
- gi No. 1871174
- % Identity 71.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 922: from 6 to 113
- Alignment No. 7934
- gi No. 1871175
- % Identity 73.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7935
- gi No. 1906607
- % Identity 75.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113

- Alignment No. 7936
- gi No. 1944203
- % Identity 80.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 922: from 2 to 102
  
- Alignment No. 7937
- gi No. 20322
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7938
- gi No. 20322
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7939
- gi No. 2072156
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7940
- gi No. 2119321
- % Identity 80.9
- Alignment Length 47
- Location of Alignment in SEQ ID NO 922: from 67 to 113
  
- Alignment No. 7941
- gi No. 2119326
- % Identity 81.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 922: from 1 to 20
  
- Alignment No. 7942
- gi No. 2129524
- % Identity 94.1
- Alignment Length 34
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 7943
- gi No. 2129524
- % Identity 86.3
- Alignment Length 95
- Location of Alignment in SEQ ID NO 922: from 21 to 115
  
- Alignment No. 7944
- gi No. 2129529
- % Identity 89.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 7945
- gi No. 2129529
- % Identity 86.3
- Alignment Length 95
- Location of Alignment in SEQ ID NO 922: from 21 to 115

- Alignment No. 7946
- gi No. 2136927
- % Identity 77.6
- Alignment Length 49
- Location of Alignment in SEQ ID NO 922: from 65 to 113
  
- Alignment No. 7947
- gi No. 223071
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7948
- gi No. 2231555
- % Identity 71.4
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7949
- gi No. 2231557
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7950
- gi No. 2231561
- % Identity 70.5
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7951
- gi No. 223390
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 922: from 1 to 26
  
- Alignment No. 7952
- gi No. 223855
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7953
- gi No. 224304
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7954
- gi No. 224305
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7955
- gi No. 224306
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7956



- gi No. 2244734
- % Identity 97.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 922: from 29 to 113
  
- Alignment No. 7957
- gi No. 225100
- % Identity 73.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7958
- gi No. 2253214
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7959
- gi No. 2253214
- % Identity 77.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7960
- gi No. 2253217
- % Identity 81.5
- Alignment Length 92
- Location of Alignment in SEQ ID NO 922: from 22 to 113
  
- Alignment No. 7961
- gi No. 2253219
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7962
- gi No. 2253219
- % Identity 73.6
- Alignment Length 129
- Location of Alignment in SEQ ID NO 922: from 1 to 113
  
- Alignment No. 7963
- gi No. 2253221
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7964
- gi No. 2253223
- % Identity 72.8
- Alignment Length 114
- Location of Alignment in SEQ ID NO 922: from 2 to 115
  
- Alignment No. 7965
- gi No. 2289966
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 922: from 80 to 113
  
- Alignment No. 7966
- gi No. 2289971

- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 922: from 80 to 113
  
- Alignment No. 7967
- gi No. 2289975
- % Identity 83.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7968
- gi No. 229690
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7969
- gi No. 2304965
- % Identity 86
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7970
- gi No. 2304969
- % Identity 76.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7971
- gi No. 231494
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7972
- gi No. 231495
- % Identity 81.6
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7973
- gi No. 231495
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7974
- gi No. 231496
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7975
- gi No. 231496
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7976
- gi No. 231498
- % Identity 90.3

- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7977
- gi No. 231499
- % Identity 81.6
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7978
- gi No. 231499
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7979
- gi No. 231501
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7980
- gi No. 231501
- % Identity 86.2
- Alignment Length 87
- Location of Alignment in SEQ ID NO 922: from 27 to 113
  
- Alignment No. 7981
- gi No. 231502
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7982
- gi No. 231502
- % Identity 95.6
- Alignment Length 68
- Location of Alignment in SEQ ID NO 922: from 21 to 88
  
- Alignment No. 7983
- gi No. 231503
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 7984
- gi No. 231503
- % Identity 93.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 7985
- gi No. 231504
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 7986
- gi No. 231504
- % Identity 82.1
- Alignment Length 112

- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 7987
- gi No. 231505
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
- Alignment No. 7988
- gi No. 231505
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 7989
- gi No. 231506
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7990
- gi No. 2315847
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7991
- gi No. 2315849
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7992
- gi No. 2318133
- % Identity 84.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7993
- gi No. 2318135
- % Identity 82.9
- Alignment Length 35
- Location of Alignment in SEQ ID NO 922: from 1 to 22
- Alignment No. 7994
- gi No. 2318135
- % Identity 84.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7995
- gi No. 2492664
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 7996
- gi No. 2492666
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113

- Alignment No. 7997
- gi No. 2492668
- % Identity 82.1
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 7998
- gi No. 2492668
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 7999
- gi No. 2492669
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 922: from 79 to 113
  
- Alignment No. 8000
- gi No. 2492670
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 922: from 89 to 113
  
- Alignment No. 8001
- gi No. 2492671
- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 922: from 79 to 113
  
- Alignment No. 8002
- gi No. 2492672
- % Identity 80.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8003
- gi No. 2492674
- % Identity 79.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8004
- gi No. 2588914
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8005
- gi No. 2624850
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8006
- gi No. 2641233
- % Identity 71
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113

- Alignment No. 8007
- gi No. 2641235
- % Identity 70.7
- Alignment Length 92
- Location of Alignment in SEQ ID NO 922: from 21 to 112
  
- Alignment No. 8008
- gi No. 2642634
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 922: from 21 to 40
  
- Alignment No. 8009
- gi No. 2665740
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8010
- gi No. 2724046
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8011
- gi No. 2829750
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8012
- gi No. 2829754
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8013
- gi No. 2829755
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8014
- gi No. 2833326
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8015
- gi No. 2887459
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8016
- gi No. 2944389
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8017

- gi No. 2944389
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8018
- gi No. 294852
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8019
- gi No. 2967678
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8020
- gi No. 2981073
- % Identity 89.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 922: from 39 to 113
  
- Alignment No. 8021
- gi No. 3036959
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8022
- gi No. 3044210
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8023
- gi No. 3046986
- % Identity 79.5
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 8024
- gi No. 3046986
- % Identity 78.7
- Alignment Length 94
- Location of Alignment in SEQ ID NO 922: from 21 to 114
  
- Alignment No. 8025
- gi No. 309090
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8026
- gi No. 3107919
- % Identity 72.3
- Alignment Length 48
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8027
- gi No. 3107919

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- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8028
- gi No. 311755
- % Identity 88
- Alignment Length 92
- Location of Alignment in SEQ ID NO 922: from 21 to 112
  
- Alignment No. 8029
- gi No. 3121741
- % Identity 76.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8030
- gi No. 3121742
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8031
- gi No. 3123181
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8032
- gi No. 3127131
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8033
- gi No. 3127133
- % Identity 72
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8034
- gi No. 3127133
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 922: from 1 to 113
  
- Alignment No. 8035
- gi No. 3127135
- % Identity 78.6
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8036
- gi No. 3127137
- % Identity 79.3
- Alignment Length 92
- Location of Alignment in SEQ ID NO 922: from 22 to 113
  
- Alignment No. 8037
- gi No. 3182886
- % Identity 88.2

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- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8038
- gi No. 3182891
- % Identity 80.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8039
- gi No. 3182892
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8040
- gi No. 3182893
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8041
- gi No. 3182894
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8042
- gi No. 3182895
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8043
- gi No. 3182896
- % Identity 83.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8044
- gi No. 3182897
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8045
- gi No. 3182898
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8046
- gi No. 3182899
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8047
- gi No. 3182902
- % Identity 91.4
- Alignment Length 93

- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8048
- gi No. 3182903
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8049
- gi No. 3182904
- % Identity 79.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8050
- gi No. 3182905
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8051
- gi No. 3182906
- % Identity 79.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8052
- gi No. 3219758
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
- Alignment No. 8053
- gi No. 3219758
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8054
- gi No. 3219759
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
- Alignment No. 8055
- gi No. 3219759
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8056
- gi No. 3219760
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
- Alignment No. 8057
- gi No. 3219760
- % Identity 93.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113

- Alignment No. 8058
- gi No. 3219761
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
- Alignment No. 8059
- gi No. 3219761
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 8060
- gi No. 3219762
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
- Alignment No. 8061
- gi No. 3219762
- % Identity 81.7
- Alignment Length 117
- Location of Alignment in SEQ ID NO 922: from 1 to 113
- Alignment No. 8062
- gi No. 3219763
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
- Alignment No. 8063
- gi No. 3219763
- % Identity 76.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 8064
- gi No. 3219764
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
- Alignment No. 8065
- gi No. 3219764
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 8066
- gi No. 3219765
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
- Alignment No. 8067
- gi No. 3219765
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113

- Alignment No. 8068
- gi No. 3219766
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 8069
- gi No. 3219766
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8070
- gi No. 3219767
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 8071
- gi No. 3219767
- % Identity 84
- Alignment Length 94
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8072
- gi No. 3219768
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 8073
- gi No. 3219768
- % Identity 83.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8074
- gi No. 3219769
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 8075
- gi No. 3219769
- % Identity 84.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8076
- gi No. 3219770
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 8077
- gi No. 3219770
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8078

- gi No. 3219771
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 8079
- gi No. 3219771
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8080
- gi No. 3219772
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 8081
- gi No. 3219772
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8082
- gi No. 3219773
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 8083
- gi No. 3219773
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8084
- gi No. 3287956
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8085
- gi No. 3287956
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8086
- gi No. 3319951
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8087
- gi No. 3328
- % Identity 72.3
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8088
- gi No. 3336984

- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8089
- gi No. 3348131
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8090
- gi No. 3386376
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8091
- gi No. 3386380
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8092
- gi No. 3386382
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8093
- gi No. 3396073
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8094
- gi No. 3420239
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8095
- gi No. 3420239
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8096
- gi No. 3421457
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8097
- gi No. 3642631
- % Identity 85.1
- Alignment Length 47
- Location of Alignment in SEQ ID NO 922: from 67 to 113
  
- Alignment No. 8098
- gi No. 3746936
- % Identity 74

- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
- Alignment No. 8099
- gi No. 3746936
- % Identity 79.5
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 8100
- gi No. 3746938
- % Identity 74
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
- Alignment No. 8101
- gi No. 3746938
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8102
- gi No. 3746940
- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
- Alignment No. 8103
- gi No. 3746940
- % Identity 79.5
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 8104
- gi No. 3746942
- % Identity 75.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 922: from 1 to 31
- Alignment No. 8105
- gi No. 3746942
- % Identity 79.5
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 8106
- gi No. 3860544
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8107
- gi No. 387082
- % Identity 72.3
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 8108
- gi No. 3879474
- % Identity 90.3
- Alignment Length 93

- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8109
- gi No. 3880219
- % Identity 84.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8110
- gi No. 3907620
- % Identity 83.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8111
- gi No. 3907622
- % Identity 77.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8112
- gi No. 3912969
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8113
- gi No. 3924630
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8114
- gi No. 398464
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 922: from 23 to 47
- Alignment No. 8115
- gi No. 399003
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 8116
- gi No. 4009328
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8117
- gi No. 409694
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 8118
- gi No. 4105262
- % Identity 87.2
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22



- Alignment No. 8119
- gi No. 4105262
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8120
- gi No. 4138667
- % Identity 77.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8121
- gi No. 4139264
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8122
- gi No. 4139264
- % Identity 86.6
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8123
- gi No. 4204812
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8124
- gi No. 4235277
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8125
- gi No. 4249564
- % Identity 79.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8126
- gi No. 4261646
- % Identity 75.5
- Alignment Length 94
- Location of Alignment in SEQ ID NO 922: from 2 to 95
  
- Alignment No. 8127
- gi No. 4261647
- % Identity 75.5
- Alignment Length 94
- Location of Alignment in SEQ ID NO 922: from 2 to 95
  
- Alignment No. 8128
- gi No. 4261859
- % Identity 82.9
- Alignment Length 35
- Location of Alignment in SEQ ID NO 922: from 1 to 22

- Alignment No. 8129
- gi No. 4376057
- % Identity 87.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 922: from 36 to 113
  
- Alignment No. 8130
- gi No. 4376177
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 922: from 35 to 113
  
- Alignment No. 8131
- gi No. 4501881
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8132
- gi No. 4501883
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8133
- gi No. 4501885
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8134
- gi No. 4501887
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8135
- gi No. 4501889
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8136
- gi No. 4512327
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 922: from 4 to 31
  
- Alignment No. 8137
- gi No. 4587217
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8138
- gi No. 461465
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8139

- gi No. 461465
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8140
- gi No. 467215
- % Identity 79.1
- Alignment Length 110
- Location of Alignment in SEQ ID NO 922: from 4 to 113
  
- Alignment No. 8141
- gi No. 4730817
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8142
- gi No. 476332
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8143
- gi No. 476768
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8144
- gi No. 477248
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8145
- gi No. 481515
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8146
- gi No. 4837604
- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 8147
- gi No. 4837604
- % Identity 70.9
- Alignment Length 110
- Location of Alignment in SEQ ID NO 922: from 4 to 113
  
- Alignment No. 8148
- gi No. 4837606
- % Identity 73.2
- Alignment Length 41
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8149
- gi No. 4837608

- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 8150
- gi No. 4837610
- % Identity 77.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8151
- gi No. 4850238
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 8152
- gi No. 4850238
- % Identity 76.9
- Alignment Length 108
- Location of Alignment in SEQ ID NO 922: from 6 to 113
  
- Alignment No. 8153
- gi No. 4850240
- % Identity 79.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8154
- gi No. 4885049
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8155
- gi No. 4887630
- % Identity 84.9
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8156
- gi No. 4902905
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8157
- gi No. 49864
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8158
- gi No. 49868
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8159
- gi No. 5031514
- % Identity 82.8

- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8160
- gi No. 5031524
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 8161
- gi No. 5031524
- % Identity 76.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8162
- gi No. 5053109
- % Identity 82.8
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8163
- gi No. 5114428
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8164
- gi No. 5230839
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8165
- gi No. 5230841
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8166
- gi No. 5230841
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8167
- gi No. 543484
- % Identity 77.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8168
- gi No. 543766
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 8169
- gi No. 543766
- % Identity 75
- Alignment Length 112

- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 8170
- gi No. 543767
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8171
- gi No. 543768
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8172
- gi No. 5578749
- % Identity 80.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8173
- gi No. 5597005
- % Identity 76.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8174
- gi No. 567192
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8175
- gi No. 5679334
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8176
- gi No. 5702223
- % Identity 72.3
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 8177
- gi No. 5702225
- % Identity 82.8
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8178
- gi No. 5702227
- % Identity 72.3
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 8179
- gi No. 5702229
- % Identity 72.3
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113

- Alignment No. 8180
- gi No. 5714751
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8181
- gi No. 5726016
- % Identity 78
- Alignment Length 41
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8182
- gi No. 5726016
- % Identity 70.9
- Alignment Length 117
- Location of Alignment in SEQ ID NO 922: from 2 to 118
  
- Alignment No. 8183
- gi No. 5726018
- % Identity 78
- Alignment Length 41
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8184
- gi No. 5726018
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8185
- gi No. 5726020
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8186
- gi No. 5726020
- % Identity 77.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8187
- gi No. 5751
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8188
- gi No. 576368
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8189
- gi No. 602958
- % Identity 78.6
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113

- Alignment No. 8190
- gi No. 627194
- % Identity 72.2
- Alignment Length 54
- Location of Alignment in SEQ ID NO 922: from 4 to 57
  
- Alignment No. 8191
- gi No. 627304
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8192
- gi No. 627834
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8193
- gi No. 63018
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8194
- gi No. 630802
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8195
- gi No. 64509
- % Identity 75.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8196
- gi No. 6628
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8197
- gi No. 683725
- % Identity 89.8
- Alignment Length 88
- Location of Alignment in SEQ ID NO 922: from 21 to 108
  
- Alignment No. 8198
- gi No. 693709
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8199
- gi No. 71611
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8200



- gi No. 71614
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8201
- gi No. 71616
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8202
- gi No. 71620
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8203
- gi No. 71621
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8204
- gi No. 71622
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8205
- gi No. 71625
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8206
- gi No. 71627
- % Identity 86
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8207
- gi No. 71629
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8208
- gi No. 71634
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8209
- gi No. 71634
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8210
- gi No. 71638

- % Identity 80
- Alignment Length 50
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8211
- gi No. 71638
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8212
- gi No. 71639
- % Identity 74.5
- Alignment Length 51
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8213
- gi No. 71639
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8214
- gi No. 7183
- % Identity 70.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8215
- gi No. 7185
- % Identity 72.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8216
- gi No. 7187
- % Identity 73.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 8217
- gi No. 7191
- % Identity 72.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 922: from 1 to 31
  
- Alignment No. 8218
- gi No. 728791
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8219
- gi No. 728792
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8220
- gi No. 728793
- % Identity 89.2

- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8221
- gi No. 728796
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8222
- gi No. 728798
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8223
- gi No. 797290
- % Identity 76.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
  
- Alignment No. 8224
- gi No. 809561
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8225
- gi No. 83999
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 8226
- gi No. 84000
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 922: from 1 to 22
  
- Alignment No. 8227
- gi No. 84082
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8228
- gi No. 84344
- % Identity 73.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8229
- gi No. 84751
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
  
- Alignment No. 8230
- gi No. 85358
- % Identity 81.7
- Alignment Length 93

- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8231
- gi No. 85495
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8232
- gi No. 86169
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8233
- gi No. 86742
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8234
- gi No. 871546
- % Identity 81.7
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8235
- gi No. 90263
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 8236
- gi No. 940010
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 922: from 21 to 113
- Alignment No. 8237
- gi No. 950002
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 922: from 2 to 113
- Alignment No. 8238
- gi No. 998468
- % Identity 100
- Alignment Length 19
- Location of Alignment in SEQ ID NO 922: from 4 to 22

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 923
- Ceres seq_id 1499213
- Location of start within SEQ ID NO 920: at 585 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8239
- Actin
- Location within SEQ ID NO 923: from 1 to 107 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8240
- gi No. 100990
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8241
- gi No. 10199
- % Identity 77
- Alignment Length 74
- Location of Alignment in SEQ ID NO 923: from 1 to 45

- Alignment No. 8242
- gi No. 102181
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 923: from 88 to 107

- Alignment No. 8243
- gi No. 1022821
- % Identity 78.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8244
- gi No. 102330
- % Identity 78.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8245
- gi No. 103061
- % Identity 89.9
- Alignment Length 89
- Location of Alignment in SEQ ID NO 923: from 19 to 107

- Alignment No. 8246
- gi No. 1064826
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 923: from 18 to 93

- Alignment No. 8247
- gi No. 1064828
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 923: from 18 to 93

- Alignment No. 8248
- gi No. 1064832
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 923: from 18 to 93

- Alignment No. 8249
- gi No. 1070613
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8250
- gi No. 1085616
- % Identity 82.5
- Alignment Length 143
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8251
- gi No. 1085617
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8252
- gi No. 113213
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8253
- gi No. 113214
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8254
- gi No. 113215
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8255
- gi No. 113216
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8256
- gi No. 113217
- % Identity 93.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 106

- Alignment No. 8257
- gi No. 113218
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8258
- gi No. 113220
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8259
- gi No. 113222
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8260

- gi No. 113223
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8261
- gi No. 113224
- % Identity 78.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8262
- gi No. 113226
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8263
- gi No. 113227
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8264
- gi No. 113228
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8265
- gi No. 113229
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8266
- gi No. 113230
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8267
- gi No. 113231
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8268
- gi No. 113232
- % Identity 81.8
- Alignment Length 165
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8269
- gi No. 113233
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8270
- gi No. 113239

- % Identity 77.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8271
- gi No. 113240
- % Identity 88.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8272
- gi No. 113241
- % Identity 74.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8273
- gi No. 113242
- % Identity 75.7
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8274
- gi No. 113243
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8275
- gi No. 113244
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8276
- gi No. 113245
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8277
- gi No. 113246
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8278
- gi No. 113247
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8279
- gi No. 113249
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8280
- gi No. 113250
- % Identity 89.1

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- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8281
- gi No. 113253
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8282
- gi No. 113254
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8283
- gi No. 113255
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8284
- gi No. 113256
- % Identity 81.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 106

- Alignment No. 8285
- gi No. 113257
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8286
- gi No. 113258
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8287
- gi No. 113261
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8288
- gi No. 113263
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8289
- gi No. 113268
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8290
- gi No. 113271
- % Identity 85.4
- Alignment Length 137

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- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8291
- gi No. 113273
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8292
- gi No. 113275
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8293
- gi No. 113276
- % Identity 75.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8294
- gi No. 113277
- % Identity 81.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8295
- gi No. 113280
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8296
- gi No. 113281
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8297
- gi No. 113282
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8298
- gi No. 113283
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8299
- gi No. 113284
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8300
- gi No. 113288
- % Identity 84
- Alignment Length 125
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8301
- gi No. 113289
- % Identity 81
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8302
- gi No. 113290
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8303
- gi No. 113291
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8304
- gi No. 113292
- % Identity 81
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8305
- gi No. 113293
- % Identity 80.1
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8306
- gi No. 113294
- % Identity 80.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8307
- gi No. 113296
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8308
- gi No. 113297
- % Identity 81.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8309
- gi No. 113300
- % Identity 74.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8310
- gi No. 113301
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8311
- gi No. 113302
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8312
- gi No. 113303
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8313
- gi No. 113304
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8314
- gi No. 113305
- % Identity 78.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8315
- gi No. 113306
- % Identity 78.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8316
- gi No. 113307
- % Identity 81.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8317
- gi No. 113308
- % Identity 89.7
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8318
- gi No. 113309
- % Identity 81.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8319
- gi No. 1168316
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8320
- gi No. 1168317
- % Identity 78.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8321

- gi No. 1168318
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8322
- gi No. 1168319
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8323
- gi No. 1168320
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8324
- gi No. 1168321
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8325
- gi No. 1168322
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8326
- gi No. 1168323
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8327
- gi No. 1168324
- % Identity 93.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8328
- gi No. 1168325
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8329
- gi No. 1168326
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8330
- gi No. 1168337
- % Identity 72.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8331
- gi No. 1168338

- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8332
- gi No. 1213444
- % Identity 84
- Alignment Length 125
- Location of Alignment in SEQ ID NO 923: from 1 to 95
  
- Alignment No. 8333
- gi No. 1304269
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8334
- gi No. 1351866
- % Identity 78.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8335
- gi No. 1351867
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8336
- gi No. 1351868
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8337
- gi No. 1351869
- % Identity 85.1
- Alignment Length 141
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8338
- gi No. 1480822
- % Identity 72.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8339
- gi No. 1480824
- % Identity 73
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8340
- gi No. 1480826
- % Identity 72.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8341
- gi No. 1498326
- % Identity 95.7

- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8342
- gi No. 1498328
- % Identity 94.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8343
- gi No. 1498330
- % Identity 92.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8344
- gi No. 1498332
- % Identity 95.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8345
- gi No. 1498334
- % Identity 94
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8346
- gi No. 1498338
- % Identity 92.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8347
- gi No. 1498340
- % Identity 92.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8348
- gi No. 1498342
- % Identity 92.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8349
- gi No. 1498344
- % Identity 93.1
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8350
- gi No. 1498346
- % Identity 94.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8351
- gi No. 1498382
- % Identity 95.7
- Alignment Length 116

- Location of Alignment in SEQ ID NO 923: from 1 to 86
- Alignment No. 8352
- gi No. 1498384
- % Identity 91.4
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
- Alignment No. 8353
- gi No. 1498386
- % Identity 92.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
- Alignment No. 8354
- gi No. 1498388
- % Identity 95.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
- Alignment No. 8355
- gi No. 1498390
- % Identity 94.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
- Alignment No. 8356
- gi No. 1498393
- % Identity 91.4
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
- Alignment No. 8357
- gi No. 1498395
- % Identity 91.4
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
- Alignment No. 8358
- gi No. 1519401
- % Identity 89
- Alignment Length 118
- Location of Alignment in SEQ ID NO 923: from 1 to 88
- Alignment No. 8359
- gi No. 1519403
- % Identity 80
- Alignment Length 45
- Location of Alignment in SEQ ID NO 923: from 1 to 15
- Alignment No. 8360
- gi No. 1519405
- % Identity 84
- Alignment Length 50
- Location of Alignment in SEQ ID NO 923: from 1 to 20
- Alignment No. 8361
- gi No. 1531672
- % Identity 94.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107



- Alignment No. 8362
- gi No. 1531674
- % Identity 95.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8363
- gi No. 156765
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8364
- gi No. 156775
- % Identity 87.3
- Alignment Length 55
- Location of Alignment in SEQ ID NO 923: from 33 to 87
  
- Alignment No. 8365
- gi No. 1575591
- % Identity 85
- Alignment Length 60
- Location of Alignment in SEQ ID NO 923: from 14 to 73
  
- Alignment No. 8366
- gi No. 158914
- % Identity 80.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8367
- gi No. 161413
- % Identity 91.8
- Alignment Length 61
- Location of Alignment in SEQ ID NO 923: from 47 to 107
  
- Alignment No. 8368
- gi No. 161424
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8369
- gi No. 161430
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8370
- gi No. 162607
- % Identity 96.8
- Alignment Length 31
- Location of Alignment in SEQ ID NO 923: from 77 to 107
  
- Alignment No. 8371
- gi No. 1666228
- % Identity 93.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8372
- gi No. 1666232
- % Identity 93.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8373
- gi No. 1666234
- % Identity 89.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8374
- gi No. 1669387
- % Identity 92.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8375
- gi No. 1669389
- % Identity 92.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8376
- gi No. 167589
- % Identity 88
- Alignment Length 83
- Location of Alignment in SEQ ID NO 923: from 25 to 107
  
- Alignment No. 8377
- gi No. 167600
- % Identity 90.2
- Alignment Length 61
- Location of Alignment in SEQ ID NO 923: from 47 to 107
  
- Alignment No. 8378
- gi No. 167605
- % Identity 87.7
- Alignment Length 65
- Location of Alignment in SEQ ID NO 923: from 43 to 107
  
- Alignment No. 8379
- gi No. 167612
- % Identity 88.5
- Alignment Length 87
- Location of Alignment in SEQ ID NO 923: from 21 to 107
  
- Alignment No. 8380
- gi No. 167642
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 923: from 20 to 107
  
- Alignment No. 8381
- gi No. 167652
- % Identity 90.7
- Alignment Length 54
- Location of Alignment in SEQ ID NO 923: from 54 to 107
  
- Alignment No. 8382

- gi No. 168404
- % Identity 84.8
- Alignment Length 138
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8383
- gi No. 1703100
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8384
- gi No. 1703101
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8385
- gi No. 1703102
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8386
- gi No. 1703103
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8387
- gi No. 1703106
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8388
- gi No. 1703107
- % Identity 88.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8389
- gi No. 1703108
- % Identity 98.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8390
- gi No. 1703109
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8391
- gi No. 1703110
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8392
- gi No. 1703111

- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8393
- gi No. 1703112
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8394
- gi No. 1703114
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8395
- gi No. 1703115
- % Identity 92.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8396
- gi No. 1703116
- % Identity 85.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8397
- gi No. 1703117
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8398
- gi No. 1703118
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8399
- gi No. 1703119
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8400
- gi No. 1703120
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8401
- gi No. 1703121
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8402
- gi No. 1703122
- % Identity 86.1

- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8403
- gi No. 1703123
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8404
- gi No. 1703124
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8405
- gi No. 1703125
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8406
- gi No. 1703127
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8407
- gi No. 1703128
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8408
- gi No. 1703129
- % Identity 93.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8409
- gi No. 1703130
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8410
- gi No. 1703131
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8411
- gi No. 1703132
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8412
- gi No. 1703133
- % Identity 86.1
- Alignment Length 137

- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8413
- gi No. 1703134
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8414
- gi No. 1703135
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8415
- gi No. 1703136
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8416
- gi No. 1703137
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8417
- gi No. 1703138
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8418
- gi No. 1703139
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8419
- gi No. 1703140
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8420
- gi No. 1703141
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8421
- gi No. 1703142
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8422
- gi No. 1703147
- % Identity 78.7
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8423
- gi No. 1703148
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8424
- gi No. 1703149
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8425
- gi No. 1703151
- % Identity 89.7
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8426
- gi No. 1703152
- % Identity 74.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8427
- gi No. 1703153
- % Identity 81.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8428
- gi No. 1703154
- % Identity 83
- Alignment Length 141
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8429
- gi No. 1703156
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8430
- gi No. 1703157
- % Identity 83
- Alignment Length 141
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8431
- gi No. 1703158
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8432
- gi No. 1703160
- % Identity 78.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8433
- gi No. 1703161
- % Identity 70.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8434
- gi No. 178067
- % Identity 82.2
- Alignment Length 90
- Location of Alignment in SEQ ID NO 923: from 1 to 60
  
- Alignment No. 8435
- gi No. 1813478
- % Identity 72.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8436
- gi No. 1871174
- % Identity 86.8
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8437
- gi No. 1882997
- % Identity 79.6
- Alignment Length 108
- Location of Alignment in SEQ ID NO 923: from 1 to 87
  
- Alignment No. 8438
- gi No. 1883024
- % Identity 83.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 923: from 1 to 87
  
- Alignment No. 8439
- gi No. 1883032
- % Identity 78.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 923: from 1 to 87
  
- Alignment No. 8440
- gi No. 1906607
- % Identity 89.7
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8441
- gi No. 20322
- % Identity 91.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8442
- gi No. 2072156
- % Identity 81.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8443



- gi No. 2119321
- % Identity 83.7
- Alignment Length 43
- Location of Alignment in SEQ ID NO 923: from 1 to 13
  
- Alignment No. 8444
- gi No. 2119323
- % Identity 80.3
- Alignment Length 71
- Location of Alignment in SEQ ID NO 923: from 1 to 64
  
- Alignment No. 8445
- gi No. 2119324
- % Identity 89.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 923: from 41 to 107
  
- Alignment No. 8446
- gi No. 2119325
- % Identity 88.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 923: from 34 to 87
  
- Alignment No. 8447
- gi No. 2119327
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 923: from 1 to 12
  
- Alignment No. 8448
- gi No. 2119330
- % Identity 91.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 923: from 61 to 107
  
- Alignment No. 8449
- gi No. 2129524
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8450
- gi No. 2129529
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8451
- gi No. 2136927
- % Identity 84.1
- Alignment Length 44
- Location of Alignment in SEQ ID NO 923: from 1 to 14
  
- Alignment No. 8452
- gi No. 2136927
- % Identity 84.7
- Alignment Length 72
- Location of Alignment in SEQ ID NO 923: from 36 to 107
  
- Alignment No. 8453
- gi No. 223071

- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8454
- gi No. 2231555
- % Identity 73.9
- Alignment Length 92
- Location of Alignment in SEQ ID NO 923: from 1 to 63
- Alignment No. 8455
- gi No. 2231557
- % Identity 76.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 923: from 1 to 63
- Alignment No. 8456
- gi No. 2231561
- % Identity 72.8
- Alignment Length 92
- Location of Alignment in SEQ ID NO 923: from 1 to 63
- Alignment No. 8457
- gi No. 223597
- % Identity 73
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8458
- gi No. 223855
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8459
- gi No. 224304
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8460
- gi No. 224305
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8461
- gi No. 224306
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8462
- gi No. 2244734
- % Identity 96.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8463
- gi No. 225100
- % Identity 78.8

- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8464
- gi No. 2253214
- % Identity 94.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8465
- gi No. 2253217
- % Identity 84.5
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8466
- gi No. 2253219
- % Identity 95.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8467
- gi No. 2253221
- % Identity 84.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8468
- gi No. 2253223
- % Identity 76.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8469
- gi No. 2289966
- % Identity 84.5
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8470
- gi No. 2289971
- % Identity 81.9
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8471
- gi No. 2289975
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8472
- gi No. 229690
- % Identity 84.3
- Alignment Length 134
- Location of Alignment in SEQ ID NO 923: from 1 to 104
  
- Alignment No. 8473
- gi No. 2304965
- % Identity 85.4
- Alignment Length 137

- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8474
- gi No. 2304969
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8475
- gi No. 231494
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8476
- gi No. 231495
- % Identity 94.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8477
- gi No. 231496
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8478
- gi No. 231498
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8479
- gi No. 231499
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8480
- gi No. 231501
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8481
- gi No. 231503
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8482
- gi No. 231504
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8483
- gi No. 231505
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8484
- gi No. 231506
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8485
- gi No. 2315847
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8486
- gi No. 2315849
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8487
- gi No. 2318133
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8488
- gi No. 2318135
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8489
- gi No. 2492664
- % Identity 84.7
- Alignment Length 118
- Location of Alignment in SEQ ID NO 923: from 1 to 88
  
- Alignment No. 8490
- gi No. 2492666
- % Identity 82
- Alignment Length 111
- Location of Alignment in SEQ ID NO 923: from 1 to 81
  
- Alignment No. 8491
- gi No. 2492667
- % Identity 96.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 923: from 76 to 107
  
- Alignment No. 8492
- gi No. 2492668
- % Identity 83
- Alignment Length 141
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8493
- gi No. 2492669
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

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- Alignment No. 8494
- gi No. 2492670
- % Identity 82.2
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99
  
- Alignment No. 8495
- gi No. 2492671
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8496
- gi No. 2492672
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8497
- gi No. 2492674
- % Identity 76.8
- Alignment Length 139
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8498
- gi No. 2588914
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8499
- gi No. 2624850
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8500
- gi No. 2641233
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 923: from 1 to 82
  
- Alignment No. 8501
- gi No. 2641235
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 923: from 1 to 82
  
- Alignment No. 8502
- gi No. 2665740
- % Identity 77.2
- Alignment Length 123
- Location of Alignment in SEQ ID NO 923: from 1 to 93
  
- Alignment No. 8503
- gi No. 2673902
- % Identity 86.8
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8504

- gi No. 2706871
- % Identity 91.1
- Alignment Length 56
- Location of Alignment in SEQ ID NO 923: from 52 to 107
  
- Alignment No. 8505
- gi No. 2724046
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8506
- gi No. 2738264
- % Identity 80
- Alignment Length 30
- Location of Alignment in SEQ ID NO 923: from 1 to 26
  
- Alignment No. 8507
- gi No. 2829750
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8508
- gi No. 2829754
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8509
- gi No. 2829755
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8510
- gi No. 2833326
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8511
- gi No. 2944389
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8512
- gi No. 294850
- % Identity 88
- Alignment Length 100
- Location of Alignment in SEQ ID NO 923: from 8 to 107
  
- Alignment No. 8513
- gi No. 294852
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8514
- gi No. 2967678

- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8515
- gi No. 2982279
- % Identity 96.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 923: from 55 to 107
  
- Alignment No. 8516
- gi No. 2996154
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 923: from 85 to 107
  
- Alignment No. 8517
- gi No. 3036959
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8518
- gi No. 3044210
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8519
- gi No. 3046986
- % Identity 77.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8520
- gi No. 309090
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8521
- gi No. 3107919
- % Identity 89.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8522
- gi No. 311755
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8523
- gi No. 3121741
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8524
- gi No. 3121742
- % Identity 85.4



- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8525
- gi No. 3123181
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8526
- gi No. 3127131
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8527
- gi No. 3127133
- % Identity 92.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8528
- gi No. 3127135
- % Identity 89.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8529
- gi No. 3127137
- % Identity 83.8
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 106
  
- Alignment No. 8530
- gi No. 3182886
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8531
- gi No. 3182891
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8532
- gi No. 3182892
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8533
- gi No. 3182893
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8534
- gi No. 3182894
- % Identity 86.1
- Alignment Length 137

- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8535
- gi No. 3182895
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8536
- gi No. 3182896
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8537
- gi No. 3182897
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8538
- gi No. 3182898
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8539
- gi No. 3182899
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8540
- gi No. 3182902
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8541
- gi No. 3182903
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8542
- gi No. 3182904
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8543
- gi No. 3182905
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8544
- gi No. 3182906
- % Identity 78.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8545
- gi No. 321010
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 923: from 22 to 35
  
- Alignment No. 8546
- gi No. 3219758
- % Identity 94.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8547
- gi No. 3219759
- % Identity 94
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8548
- gi No. 3219760
- % Identity 94.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8549
- gi No. 3219761
- % Identity 94
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8550
- gi No. 3219762
- % Identity 94
- Alignment Length 117
- Location of Alignment in SEQ ID NO 923: from 1 to 87
  
- Alignment No. 8551
- gi No. 3219763
- % Identity 91.4
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8552
- gi No. 3219764
- % Identity 94.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8553
- gi No. 3219765
- % Identity 96.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8554
- gi No. 3219766
- % Identity 94
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86

- Alignment No. 8555
- gi No. 3219767
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 923: from 1 to 85
  
- Alignment No. 8556
- gi No. 3219768
- % Identity 95.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8557
- gi No. 3219769
- % Identity 94.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8558
- gi No. 3219770
- % Identity 89.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8559
- gi No. 3219771
- % Identity 93.1
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8560
- gi No. 3219772
- % Identity 95.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8561
- gi No. 3219773
- % Identity 94
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
  
- Alignment No. 8562
- gi No. 3249717
- % Identity 79.6
- Alignment Length 98
- Location of Alignment in SEQ ID NO 923: from 1 to 68
  
- Alignment No. 8563
- gi No. 3287956
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8564
- gi No. 3319951
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8565

- gi No. 3328
- % Identity 80.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8566
- gi No. 3336984
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8567
- gi No. 3348131
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8568
- gi No. 3386376
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8569
- gi No. 3386380
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8570
- gi No. 3386382
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8571
- gi No. 3396073
- % Identity 83.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 923: from 1 to 85
  
- Alignment No. 8572
- gi No. 3420239
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8573
- gi No. 3421457
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8574
- gi No. 3550350
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8575
- gi No. 3642631

- % Identity 80.7
- Alignment Length 88
- Location of Alignment in SEQ ID NO 923: from 1 to 59
  
- Alignment No. 8576
- gi No. 3746936
- % Identity 89.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8577
- gi No. 3746938
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8578
- gi No. 3746940
- % Identity 91.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8579
- gi No. 3746942
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8580
- gi No. 3860317
- % Identity 96.1
- Alignment Length 103
- Location of Alignment in SEQ ID NO 923: from 5 to 107
  
- Alignment No. 8581
- gi No. 3860544
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8582
- gi No. 387082
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8583
- gi No. 3879474
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8584
- gi No. 3880219
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8585
- gi No. 3907620
- % Identity 81

- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8586
- gi No. 3907622
- % Identity 76.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8587
- gi No. 3912969
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8588
- gi No. 3924630
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8589
- gi No. 399003
- % Identity 82.3
- Alignment Length 141
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8590
- gi No. 4009328
- % Identity 83.7
- Alignment Length 49
- Location of Alignment in SEQ ID NO 923: from 1 to 19
  
- Alignment No. 8591
- gi No. 409694
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8592
- gi No. 4105262
- % Identity 91.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8593
- gi No. 4139264
- % Identity 97.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8594
- gi No. 4204812
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8595
- gi No. 4220623
- % Identity 85.8
- Alignment Length 120

- Location of Alignment in SEQ ID NO 923: from 1 to 90
- Alignment No. 8596
- gi No. 4235277
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8597
- gi No. 4249564
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8598
- gi No. 4376057
- % Identity 83.8
- Alignment Length 105
- Location of Alignment in SEQ ID NO 923: from 1 to 75
- Alignment No. 8599
- gi No. 4490385
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8600
- gi No. 4501881
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8601
- gi No. 4501883
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8602
- gi No. 4501885
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8603
- gi No. 4501887
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8604
- gi No. 4501889
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8605
- gi No. 4574288
- % Identity 86.3
- Alignment Length 131
- Location of Alignment in SEQ ID NO 923: from 1 to 107



- Alignment No. 8606
- gi No. 4587217
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8607
- gi No. 461465
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8608
- gi No. 467215
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8609
- gi No. 4691448
- % Identity 93.6
- Alignment Length 94
- Location of Alignment in SEQ ID NO 923: from 1 to 71
  
- Alignment No. 8610
- gi No. 476332
- % Identity 84.9
- Alignment Length 119
- Location of Alignment in SEQ ID NO 923: from 1 to 89
  
- Alignment No. 8611
- gi No. 476768
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8612
- gi No. 477248
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8613
- gi No. 481515
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8614
- gi No. 482262
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 923: from 48 to 65
  
- Alignment No. 8615
- gi No. 482696
- % Identity 81.3
- Alignment Length 113
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8616
- gi No. 4837604
- % Identity 75.2
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99
  
- Alignment No. 8617
- gi No. 4837606
- % Identity 77.5
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99
  
- Alignment No. 8618
- gi No. 4837610
- % Identity 72.1
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99
  
- Alignment No. 8619
- gi No. 4850238
- % Identity 75.2
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99
  
- Alignment No. 8620
- gi No. 4850240
- % Identity 77.5
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99
  
- Alignment No. 8621
- gi No. 4885049
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8622
- gi No. 4887630
- % Identity 81
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8623
- gi No. 4902905
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8624
- gi No. 49864
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8625
- gi No. 49868
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8626

- gi No. 5031514
- % Identity 80
- Alignment Length 135
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8627
- gi No. 5031524
- % Identity 73.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 106
  
- Alignment No. 8628
- gi No. 5053109
- % Identity 79.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8629
- gi No. 5114428
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8630
- gi No. 5230839
- % Identity 78.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8631
- gi No. 5230841
- % Identity 97.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8632
- gi No. 543484
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8633
- gi No. 543766
- % Identity 82.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8634
- gi No. 543767
- % Identity 77.1
- Alignment Length 144
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8635
- gi No. 543768
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8636
- gi No. 544861

- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8637
- gi No. 55675
- % Identity 88
- Alignment Length 25
- Location of Alignment in SEQ ID NO 923: from 83 to 107
  
- Alignment No. 8638
- gi No. 5578749
- % Identity 71.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 923: from 1 to 16
  
- Alignment No. 8639
- gi No. 5597005
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8640
- gi No. 567192
- % Identity 84.9
- Alignment Length 119
- Location of Alignment in SEQ ID NO 923: from 1 to 89
  
- Alignment No. 8641
- gi No. 5702223
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8642
- gi No. 5702225
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8643
- gi No. 5702227
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8644
- gi No. 5702229
- % Identity 86.5
- Alignment Length 89
- Location of Alignment in SEQ ID NO 923: from 19 to 107
  
- Alignment No. 8645
- gi No. 5714394
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 923: from 71 to 107
  
- Alignment No. 8646
- gi No. 5726016
- % Identity 94.1

- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8647
- gi No. 5726018
- % Identity 94.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8648
- gi No. 5726020
- % Identity 87.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8649
- gi No. 5751
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8650
- gi No. 576368
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8651
- gi No. 602958
- % Identity 92
- Alignment Length 50
- Location of Alignment in SEQ ID NO 923: from 1 to 20
  
- Alignment No. 8652
- gi No. 627304
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8653
- gi No. 627834
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8654
- gi No. 63018
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8655
- gi No. 630802
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8656
- gi No. 631529
- % Identity 76.3
- Alignment Length 97

- Location of Alignment in SEQ ID NO 923: from 9 to 105
- Alignment No. 8657
- gi No. 64509
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8658
- gi No. 6628
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8659
- gi No. 693709
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8660
- gi No. 71611
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8661
- gi No. 71614
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8662
- gi No. 71616
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8663
- gi No. 71620
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8664
- gi No. 71621
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8665
- gi No. 71622
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8666
- gi No. 71625
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8667
- gi No. 71627
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8668
- gi No. 71629
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8669
- gi No. 71634
- % Identity 90.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8670
- gi No. 71638
- % Identity 91.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8671
- gi No. 71639
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8672
- gi No. 728791
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8673
- gi No. 728792
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8674
- gi No. 728793
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8675
- gi No. 728796
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8676
- gi No. 728798
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8677
- gi No. 797290
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8678
- gi No. 809561
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8679
- gi No. 818016
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 923: from 15 to 107
  
- Alignment No. 8680
- gi No. 825616
- % Identity 86.2
- Alignment Length 123
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8681
- gi No. 83999
- % Identity 71.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8682
- gi No. 84000
- % Identity 71.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8683
- gi No. 84082
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8684
- gi No. 84344
- % Identity 78.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8685
- gi No. 84751
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8686
- gi No. 84879
- % Identity 88.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8687



- gi No. 84880
- % Identity 92.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 923: from 55 to 107
  
- Alignment No. 8688
- gi No. 85358
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8689
- gi No. 85495
- % Identity 81.1
- Alignment Length 90
- Location of Alignment in SEQ ID NO 923: from 1 to 60
  
- Alignment No. 8690
- gi No. 86169
- % Identity 80.6
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99
  
- Alignment No. 8691
- gi No. 86742
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8692
- gi No. 871546
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8693
- gi No. 90263
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
  
- Alignment No. 8694
- gi No. 91918
- % Identity 95.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 923: from 66 to 107
  
- Alignment No. 8695
- gi No. 950002
- % Identity 81.6
- Alignment Length 87
- Location of Alignment in SEQ ID NO 923: from 1 to 57

Maximum Length Sequence corresponding to clone ID 159438

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 924
- Ceres seq\_id 1499214

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 925
- Ceres seq\_id 1499215
- Location of start within SEQ ID NO 924: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8696
- EF hand
- Location within SEQ ID NO 925: from 40 to 68 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 926
- Ceres seq\_id 1499216
- Location of start within SEQ ID NO 924: at 437 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8697
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 926: from 15 to 66 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8698
- gi No. 2129684
- % Identity 79.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 926: from 15 to 48
- Alignment No. 8699
- gi No. 2827715
- % Identity 82.6
- Alignment Length 163
- Location of Alignment in SEQ ID NO 926: from 15 to 175

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 927
- Ceres seq\_id 1499217
- Location of start within SEQ ID NO 924: at 446 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8700
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 927: from 12 to 63 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8701
- gi No. 2129684
- % Identity 79.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 927: from 12 to 45
- Alignment No. 8702
- gi No. 2827715
- % Identity 82.6
- Alignment Length 163
- Location of Alignment in SEQ ID NO 927: from 12 to 172

Maximum Length Sequence corresponding to clone ID 159568

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 928
- Ceres seq\_id 1499218

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 929
- Ceres seq\_id 1499219
- Location of start within SEQ ID NO 928: at 305 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8703
- Tetrapyrrole (Corrin/Porphyrin) Methylases.
- Location within SEQ ID NO 929: from 116 to 329 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8704
- gi No. 1146165
- % Identity 100
- Alignment Length 369
- Location of Alignment in SEQ ID NO 929: from 1 to 369
- Alignment No. 8705
- gi No. 1490606
- % Identity 99.2
- Alignment Length 369
- Location of Alignment in SEQ ID NO 929: from 1 to 369
- Alignment No. 8706
- gi No. 1531541
- % Identity 73.1
- Alignment Length 334
- Location of Alignment in SEQ ID NO 929: from 35 to 368

Maximum Length Sequence corresponding to clone ID 159614

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 930
- Ceres seq\_id 1499220

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 931
- Ceres seq\_id 1499221
- Location of start within SEQ ID NO 930: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8707
- SRP54-type protein
- Location within SEQ ID NO 931: from 146 to 427 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8708
- gi No. 2911886
- % Identity 70.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 931: from 296 to 427

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 932
- Ceres seq\_id 1499222
- Location of start within SEQ ID NO 930: at 270 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8709
- SRP54-type protein

- Location within SEQ ID NO 932: from 57 to 338 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8710
- gi No. 2911886
- % Identity 70.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 932: from 207 to 338

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 933
- Ceres seq\_id 1499223
- Location of start within SEQ ID NO 930: at 273 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8711
- SRP54-type protein
- Location within SEQ ID NO 933: from 56 to 337 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8712
- gi No. 2911886
- % Identity 70.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 933: from 206 to 337

Maximum Length Sequence corresponding to clone ID 205489

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 934
- Ceres seq\_id 1499224

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 935
- Ceres seq\_id 1499225
- Location of start within SEQ ID NO 934: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8713
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 935: from 18 to 124 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8714
- gi No. 2498731
- % Identity 84.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 935: from 1 to 124
- Alignment No. 8715
- gi No. 2498732
- % Identity 97.6
- Alignment Length 125
- Location of Alignment in SEQ ID NO 935: from 1 to 124

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 936
- Ceres seq\_id 1499226
- Location of start within SEQ ID NO 934: at 302 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8716
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 936: from 1 to 72 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8717
- gi No. 2498731
- % Identity 84.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 936: from 1 to 72
- Alignment No. 8718
- gi No. 2498732
- % Identity 97.6
- Alignment Length 125
- Location of Alignment in SEQ ID NO 936: from 1 to 72

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 937
- Ceres seq\_id 1499227
- Location of start within SEQ ID NO 934: at 314 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8719
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 937: from 1 to 68 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8720
- gi No. 2498731
- % Identity 84.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 937: from 1 to 68
- Alignment No. 8721
- gi No. 2498732
- % Identity 97.6
- Alignment Length 125
- Location of Alignment in SEQ ID NO 937: from 1 to 68

Maximum Length Sequence corresponding to clone ID 205976

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 938
- Ceres seq\_id 1499228

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 939
- Ceres seq\_id 1499229
- Location of start within SEQ ID NO 938: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8722
- gi No. 4836868
- % Identity 98.8
- Alignment Length 509
- Location of Alignment in SEQ ID NO 939: from 20 to 528

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 940
- Ceres seq\_id 1499230
- Location of start within SEQ ID NO 938: at 59 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8723
- gi No. 4836868
- % Identity 98.8
- Alignment Length 509
- Location of Alignment in SEQ ID NO 940: from 1 to 509

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 941
- Ceres seq\_id 1499231
- Location of start within SEQ ID NO 938: at 374 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8724
- gi No. 4836868
- % Identity 98.8
- Alignment Length 509
- Location of Alignment in SEQ ID NO 941: from 1 to 404

Maximum Length Sequence corresponding to clone ID 206045

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 942
- Ceres seq\_id 1499232

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 943
- Ceres seq\_id 1499233
- Location of start within SEQ ID NO 942: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8725
- Mucin-like glycoprotein
- Location within SEQ ID NO 943: from 8 to 89 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 206237

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 944
- Ceres seq\_id 1499242

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 945
- Ceres seq\_id 1499243
- Location of start within SEQ ID NO 944: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8726
- Pectinesterase
- Location within SEQ ID NO 945: from 70 to 123 aa.

(D) Related Amino Acid Sequences

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(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 946
- Ceres seq\_id 1499244
- Location of start within SEQ ID NO 944: at 872 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 947
- Ceres seq\_id 1499245
- Location of start within SEQ ID NO 944: at 995 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 206518

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 948
- Ceres seq\_id 1499250

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 949
- Ceres seq\_id 1499251
- Location of start within SEQ ID NO 948: at 125 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8727
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 949: from 102 to 404 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8728
- gi No. 2911716
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 949: from 377 to 387

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 950
- Ceres seq\_id 1499252
- Location of start within SEQ ID NO 948: at 287 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8729
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 950: from 48 to 350 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8730
- gi No. 2911716
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 950: from 323 to 333

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 951

- Ceres seq\_id 1499253
- Location of start within SEQ ID NO 948: at 356 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8731
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 951: from 25 to 327 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8732
- gi No. 2911716
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 951: from 300 to 310

Maximum Length Sequence corresponding to clone ID 207043

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 952
- Ceres seq\_id 1499254

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 953
- Ceres seq\_id 1499255
- Location of start within SEQ ID NO 952: at 23 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8733
- gi No. 1946364
- % Identity 100
- Alignment Length 447
- Location of Alignment in SEQ ID NO 953: from 83 to 529

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 954
- Ceres seq\_id 1499256
- Location of start within SEQ ID NO 952: at 269 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8734
- gi No. 1946364
- % Identity 100
- Alignment Length 447
- Location of Alignment in SEQ ID NO 954: from 1 to 447

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 955
- Ceres seq\_id 1499257
- Location of start within SEQ ID NO 952: at 374 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8735
- gi No. 1946364
- % Identity 100
- Alignment Length 447
- Location of Alignment in SEQ ID NO 955: from 1 to 412



Maximum Length Sequence corresponding to clone ID 207137

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 956
- Ceres seq\_id 1499258

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 957
- Ceres seq\_id 1499259
- Location of start within SEQ ID NO 956: at 65 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8736
- L1P family of ribosomal proteins
- Location within SEQ ID NO 957: from 124 to 329 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8737
- gi No. 1350625
- % Identity 79.5
- Alignment Length 176
- Location of Alignment in SEQ ID NO 957: from 89 to 264

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 958
- Ceres seq\_id 1499260
- Location of start within SEQ ID NO 956: at 95 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8738
- L1P family of ribosomal proteins
- Location within SEQ ID NO 958: from 114 to 319 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8739
- gi No. 1350625
- % Identity 79.5
- Alignment Length 176
- Location of Alignment in SEQ ID NO 958: from 79 to 254

Maximum Length Sequence corresponding to clone ID 207419

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 959
- Ceres seq\_id 1499261

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 960
- Ceres seq\_id 1499262
- Location of start within SEQ ID NO 959: at 74 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8740
- Zinc finger C-x8-C-x5-C-x3-H type (and similar).
- Location within SEQ ID NO 960: from 235 to 262 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 961
- Ceres seq\_id 1499263

- Location of start within SEQ ID NO 959: at 395 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8741
- Zinc finger C-x8-C-x5-C-x3-H type (and similar).
- Location within SEQ ID NO 961: from 128 to 155 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 207558

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 962
- Ceres seq\_id 1499264

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 963
- Ceres seq\_id 1499265
- Location of start within SEQ ID NO 962: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8742
- Adhesion lipoprotein
- Location within SEQ ID NO 963: from 182 to 232 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8743
- gi No. 1001307
- % Identity 70.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 963: from 184 to 210
- Alignment No. 8744
- gi No. 2983552
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 963: from 210 to 220
- Alignment No. 8745
- gi No. 3510254
- % Identity 100
- Alignment Length 398
- Location of Alignment in SEQ ID NO 963: from 1 to 398
- Alignment No. 8746
- gi No. 3560024
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 963: from 181 to 198
- Alignment No. 8747
- gi No. 4206640
- % Identity 98
- Alignment Length 398
- Location of Alignment in SEQ ID NO 963: from 1 to 398
- Alignment No. 8748
- gi No. 4584498
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 963: from 181 to 195

- ```
- Alignment No. 8749
- gi No. 539415
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 963: from 181 to 196

- Alignment No. 8750
- gi No. 539415
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 963: from 182 to 198
```

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 964
- Ceres seq_id 1499266
- Location of start within SEQ ID NO 962: at 258 nt.
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(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8751
- Adhesion lipoprotein
- Location within SEQ ID NO 964: from 128 to 178 aa.

#### (D) Related Amino Acid Sequences

- ```
- Alignment No. 8752
- gi No. 1001307
- % Identity 70.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 964: from 130 to 156

- Alignment No. 8753
- gi No. 2983552
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 964: from 156 to 166

- Alignment No. 8754
- gi No. 3510254
- % Identity 100
- Alignment Length 398
- Location of Alignment in SEQ ID NO 964: from 1 to 344

- Alignment No. 8755
- gi No. 3560024
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 964: from 127 to 144

- Alignment No. 8756
- gi No. 4206640
- % Identity 98
- Alignment Length 398
- Location of Alignment in SEQ ID NO 964: from 1 to 344

- Alignment No. 8757
- gi No. 4584498
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 964: from 127 to 141
```

- Alignment No. 8758
- gi No. 539415
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 964: from 127 to 142

- Alignment No. 8759
- gi No. 539415
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 964: from 128 to 144

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 965
- Ceres seq_id 1499267
- Location of start within SEQ ID NO 962: at 300 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8760
- Adhesion lipoprotein
- Location within SEQ ID NO 965: from 114 to 164 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8761
- gi No. 1001307
- % Identity 70.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 965: from 116 to 142
- Alignment No. 8762
- gi No. 2983552
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 965: from 142 to 152
- Alignment No. 8763
- gi No. 3510254
- % Identity 100
- Alignment Length 398
- Location of Alignment in SEQ ID NO 965: from 1 to 330
- Alignment No. 8764
- gi No. 3560024
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 965: from 113 to 130
- Alignment No. 8765
- gi No. 4206640
- % Identity 98
- Alignment Length 398
- Location of Alignment in SEQ ID NO 965: from 1 to 330
- Alignment No. 8766
- gi No. 4584498
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 965: from 113 to 127
- Alignment No. 8767

- gi No. 539415
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 965: from 113 to 128
- Alignment No. 8768
- gi No. 539415
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 965: from 114 to 130

Maximum Length Sequence corresponding to clone ID 218944

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 966
- Ceres seq_id 1499310

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 967
- Ceres seq_id 1499311
- Location of start within SEQ ID NO 966: at 202 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8769
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 967: from 40 to 109 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 968
- Ceres seq_id 1499312
- Location of start within SEQ ID NO 966: at 232 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8770
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 968: from 30 to 99 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 969
- Ceres seq_id 1499313
- Location of start within SEQ ID NO 966: at 256 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8771
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 969: from 22 to 91 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 219286

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 970
- Ceres seq_id 1499314

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 971
- Ceres seq_id 1499315

- Location of start within SEQ ID NO 970: at 155 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8772
- 60s Acidic ribosomal protein
- Location within SEQ ID NO 971: from 73 to 129 aa.
- Alignment No. 8773
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 971: from 64 to 167 aa.
- Alignment No. 8774
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 971: from 75 to 171 aa.
- Alignment No. 8775
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 971: from 99 to 171 aa.
- Alignment No. 8776
- Syndecan domain
- Location within SEQ ID NO 971: from 1 to 142 aa.
- Alignment No. 8777
- 11-S plant seed storage protein
- Location within SEQ ID NO 971: from 76 to 170 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8778
- gi No. 482700
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 971: from 151 to 161

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 972
- Ceres seq_id 1499316
- Location of start within SEQ ID NO 970: at 266 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8779
- 60s Acidic ribosomal protein
- Location within SEQ ID NO 972: from 36 to 92 aa.
- Alignment No. 8780
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 972: from 27 to 130 aa.
- Alignment No. 8781
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 972: from 38 to 134 aa.
- Alignment No. 8782
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 972: from 62 to 134 aa.
- Alignment No. 8783
- Syndecan domain
- Location within SEQ ID NO 972: from 1 to 105 aa.

- Alignment No. 8784
- 11-S plant seed storage protein
- Location within SEQ ID NO 972: from 39 to 133 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8785
- gi No. 482700
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 972: from 114 to 124

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 973
- Ceres seq_id 1499317
- Location of start within SEQ ID NO 970: at 285 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 219894

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 974
- Ceres seq_id 1499344

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 975
- Ceres seq_id 1499345
- Location of start within SEQ ID NO 974: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 976
- Ceres seq_id 1499346
- Location of start within SEQ ID NO 974: at 90 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8786
- gi No. 3108209
- % Identity 78.8
- Alignment Length 179
- Location of Alignment in SEQ ID NO 976: from 35 to 213

Maximum Length Sequence corresponding to clone ID 220920

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 977
- Ceres seq_id 1499353

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 978
- Ceres seq_id 1499354
- Location of start within SEQ ID NO 977: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8787

- gi No. 129805
- % Identity 72.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 978: from 28 to 56

- Alignment No. 8788
- gi No. 1491776
- % Identity 75.9
- Alignment Length 29
- Location of Alignment in SEQ ID NO 978: from 28 to 56

- Alignment No. 8789
- gi No. 1633130
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 978: from 31 to 56

- Alignment No. 8790
- gi No. 520570
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 978: from 24 to 55

Maximum Length Sequence corresponding to clone ID 221164

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 979
- Ceres seq_id 1499362

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 980
- Ceres seq_id 1499363
- Location of start within SEQ ID NO 979: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 981
- Ceres seq_id 1499364
- Location of start within SEQ ID NO 979: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8791
- EF hand
- Location within SEQ ID NO 981: from 45 to 73 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8792
- gi No. 115480
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80

- Alignment No. 8793
- gi No. 115500
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80

- Alignment No. 8794

- gi No. 115534
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80

- Alignment No. 8795
- gi No. 16225
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80

- Alignment No. 8796
- gi No. 167676
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80

- Alignment No. 8797
- gi No. 189020
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 981: from 70 to 80

- Alignment No. 8798
- gi No. 189022
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 981: from 70 to 80

- Alignment No. 8799
- gi No. 2119353
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 981: from 37 to 80

- Alignment No. 8800
- gi No. 2129557
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 981: from 38 to 61

- Alignment No. 8801
- gi No. 2267084
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80

- Alignment No. 8802
- gi No. 228408
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 981: from 46 to 80

- Alignment No. 8803
- gi No. 4379369
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 981: from 37 to 80

- Alignment No. 8804
- gi No. 71673

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- ```
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 981: from 37 to 80
```

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 982
- Ceres seq\_id 1499365
- Location of start within SEQ ID NO 979: at 98 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8805
- EF hand
- Location within SEQ ID NO 982: from 13 to 41 aa.

#### (D) Related Amino Acid Sequences

- Alignment No. 8806
- gi No. 115480
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
- Alignment No. 8807
- gi No. 115500
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
- Alignment No. 8808
- gi No. 115534
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
- Alignment No. 8809
- gi No. 16225
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
- Alignment No. 8810
- gi No. 167676
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
- Alignment No. 8811
- gi No. 189020
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 982: from 38 to 48
- Alignment No. 8812
- gi No. 189022
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 982: from 38 to 48
- Alignment No. 8813
- gi No. 2119353
- % Identity 70.5

- Alignment Length 44
- Location of Alignment in SEQ ID NO 982: from 5 to 48
- Alignment No. 8814
- gi No. 2129557
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 982: from 6 to 29
- Alignment No. 8815
- gi No. 2267084
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
- Alignment No. 8816
- gi No. 228408
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 982: from 14 to 48
- Alignment No. 8817
- gi No. 4379369
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 982: from 5 to 48
- Alignment No. 8818
- gi No. 71673
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 982: from 5 to 48

Maximum Length Sequence corresponding to clone ID 221169

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 983
- Ceres seq\_id 1499370

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 984
- Ceres seq\_id 1499371
- Location of start within SEQ ID NO 983: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8819
- gi No. 1070652
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 984: from 68 to 81
- Alignment No. 8820
- gi No. 131007
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 984: from 68 to 81
- Alignment No. 8821
- gi No. 350218
- % Identity 71.4
- Alignment Length 14

- Location of Alignment in SEQ ID NO 984: from 68 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 985
- Ceres seq\_id 1499372
- Location of start within SEQ ID NO 983: at 455 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 986
- Ceres seq\_id 1499373
- Location of start within SEQ ID NO 983: at 473 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 221212

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 987
- Ceres seq\_id 1499380

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 988
- Ceres seq\_id 1499381
- Location of start within SEQ ID NO 987: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8822
- ADP-ribosylation factor family
- Location within SEQ ID NO 988: from 54 to 230 aa.
- Alignment No. 8823
- Ras family
- Location within SEQ ID NO 988: from 70 to 219 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 989
- Ceres seq\_id 1499382
- Location of start within SEQ ID NO 987: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8824
- ADP-ribosylation factor family
- Location within SEQ ID NO 989: from 5 to 181 aa.
- Alignment No. 8825
- Ras family
- Location within SEQ ID NO 989: from 21 to 170 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 990
- Ceres seq\_id 1499383

- Location of start within SEQ ID NO 987: at 207 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8826
- ADP-ribosylation factor family
- Location within SEQ ID NO 990: from 1 to 162 aa.
- Alignment No. 8827
- Ras family
- Location within SEQ ID NO 990: from 2 to 151 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 221234

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 991
- Ceres seq\_id 1499384

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 992
- Ceres seq\_id 1499385
- Location of start within SEQ ID NO 991: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8828
- Papain family cysteine protease
- Location within SEQ ID NO 992: from 123 to 158 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8829
- gi No. 108585
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 992: from 122 to 141
- Alignment No. 8830
- gi No. 1093503
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
- Alignment No. 8831
- gi No. 115738
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
- Alignment No. 8832
- gi No. 1340178
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
- Alignment No. 8833
- gi No. 1498185
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
- Alignment No. 8834

- gi No. 162042
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 992: from 141 to 159
  
- Alignment No. 8835
- gi No. 162044
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 992: from 141 to 161
  
- Alignment No. 8836
- gi No. 1705639
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
  
- Alignment No. 8837
- gi No. 1911708
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 992: from 141 to 159
  
- Alignment No. 8838
- gi No. 2144502
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
  
- Alignment No. 8839
- gi No. 2146900
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
  
- Alignment No. 8840
- gi No. 2665820
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 992: from 141 to 158
  
- Alignment No. 8841
- gi No. 2706547
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
  
- Alignment No. 8842
- gi No. 2914174
- % Identity 75
- Alignment Length 36
- Location of Alignment in SEQ ID NO 992: from 127 to 162
  
- Alignment No. 8843
- gi No. 3929737
- % Identity 78.6
- Alignment Length 28
- Location of Alignment in SEQ ID NO 992: from 135 to 162
  
- Alignment No. 8844
- gi No. 3929819

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- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 992: from 144 to 157
  
- Alignment No. 8845
- gi No. 419920
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 992: from 141 to 159
  
- Alignment No. 8846
- gi No. 452254
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 992: from 141 to 162
  
- Alignment No. 8847
- gi No. 541900
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 992: from 128 to 157

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 993
- Ceres seq\_id 1499386
- Location of start within SEQ ID NO 991: at 26 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8848
- Papain family cysteine protease
- Location within SEQ ID NO 993: from 115 to 150 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8849
- gi No. 108585
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 993: from 114 to 133
  
- Alignment No. 8850
- gi No. 1093503
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
  
- Alignment No. 8851
- gi No. 115738
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
  
- Alignment No. 8852
- gi No. 1340178
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
  
- Alignment No. 8853
- gi No. 1498185
- % Identity 71.1

- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
  
- Alignment No. 8854
- gi No. 162042
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 993: from 133 to 151
  
- Alignment No. 8855
- gi No. 162044
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 993: from 133 to 153
  
- Alignment No. 8856
- gi No. 1705639
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
  
- Alignment No. 8857
- gi No. 1911708
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 993: from 133 to 151
  
- Alignment No. 8858
- gi No. 2144502
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
  
- Alignment No. 8859
- gi No. 2146900
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
  
- Alignment No. 8860
- gi No. 2665820
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 993: from 133 to 150
  
- Alignment No. 8861
- gi No. 2706547
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
  
- Alignment No. 8862
- gi No. 2914174
- % Identity 75
- Alignment Length 36
- Location of Alignment in SEQ ID NO 993: from 119 to 154
  
- Alignment No. 8863
- gi No. 3929737
- % Identity 78.6
- Alignment Length 28



- Location of Alignment in SEQ ID NO 993: from 127 to 154
- Alignment No. 8864
- gi No. 3929819
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 993: from 136 to 149
- Alignment No. 8865
- gi No. 419920
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 993: from 133 to 151
- Alignment No. 8866
- gi No. 452254
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 993: from 133 to 154
- Alignment No. 8867
- gi No. 541900
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 993: from 120 to 149

Maximum Length Sequence corresponding to clone ID 222003

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 994
- Ceres seq\_id 1499389

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 995
- Ceres seq\_id 1499390
- Location of start within SEQ ID NO 994: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8868
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 995: from 86 to 145 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 996
- Ceres seq\_id 1499391
- Location of start within SEQ ID NO 994: at 157 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8869
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 996: from 34 to 93 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 222544

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 997
- Ceres seq\_id 1499402

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 998
- Ceres seq\_id 1499403
- Location of start within SEQ ID NO 997: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8870
- gi No. 400249
- % Identity 94.4
- Alignment Length 36
- Location of Alignment in SEQ ID NO 998: from 17 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 999
- Ceres seq\_id 1499404
- Location of start within SEQ ID NO 997: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1000
- Ceres seq\_id 1499405
- Location of start within SEQ ID NO 997: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8871
- gi No. 400249
- % Identity 94.4
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1000: from 1 to 36

Maximum Length Sequence corresponding to clone ID 222547

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1001
- Ceres seq\_id 1499406

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1002
- Ceres seq\_id 1499407
- Location of start within SEQ ID NO 1001: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8872
- gi No. 4204294
- % Identity 75.1
- Alignment Length 198
- Location of Alignment in SEQ ID NO 1002: from 54 to 247

Maximum Length Sequence corresponding to clone ID 223028

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1003
- Ceres seq\_id 1499408

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1004
- Ceres seq\_id 1499409

- Location of start within SEQ ID NO 1003: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1005
- Ceres seq\_id 1499410
- Location of start within SEQ ID NO 1003: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8873
- gi No. 5042457
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1005: from 15 to 80

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1006
- Ceres seq\_id 1499411
- Location of start within SEQ ID NO 1003: at 45 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8874
- gi No. 5042457
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1006: from 1 to 66

Maximum Length Sequence corresponding to clone ID 225428

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1007
- Ceres seq\_id 1499412

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1008
- Ceres seq\_id 1499413
- Location of start within SEQ ID NO 1007: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1009
- Ceres seq\_id 1499414
- Location of start within SEQ ID NO 1007: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8875
- gi No. 113003
- % Identity 95.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1009: from 18 to 41

- Alignment No. 8876
- gi No. 168397
- % Identity 95.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1009: from 18 to 41
  
- Alignment No. 8877
- gi No. 168422
- % Identity 100
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1009: from 18 to 41

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1010
- Ceres seq\_id 1499415
- Location of start within SEQ ID NO 1007: at 54 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8878
- gi No. 113003
- % Identity 95.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1010: from 1 to 24
  
- Alignment No. 8879
- gi No. 168397
- % Identity 95.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1010: from 1 to 24
  
- Alignment No. 8880
- gi No. 168422
- % Identity 100
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1010: from 1 to 24

Maximum Length Sequence corresponding to clone ID 225429

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1011
- Ceres seq\_id 1499416

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1012
- Ceres seq\_id 1499417
- Location of start within SEQ ID NO 1011: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1013
- Ceres seq\_id 1499418
- Location of start within SEQ ID NO 1011: at 105 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8881
- S-adenosylmethionine synthetase
- Location within SEQ ID NO 1013: from 5 to 95 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8882
- gi No. 1076485
- % Identity 92.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1013: from 3 to 84
  
- Alignment No. 8883
- gi No. 1170936
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8884
- gi No. 1170937
- % Identity 89.7
- Alignment Length 97
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
  
- Alignment No. 8885
- gi No. 1170938
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8886
- gi No. 1170939
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8887
- gi No. 127041
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8888
- gi No. 127045
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8889
- gi No. 127046
- % Identity 87.6
- Alignment Length 97
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
  
- Alignment No. 8890
- gi No. 1346520
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8891
- gi No. 1346523
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95

- Alignment No. 8892
- gi No. 1346524
- % Identity 93.6
- Alignment Length 94
- Location of Alignment in SEQ ID NO 1013: from 3 to 95
  
- Alignment No. 8893
- gi No. 1346525
- % Identity 70.2
- Alignment Length 94
- Location of Alignment in SEQ ID NO 1013: from 3 to 95
  
- Alignment No. 8894
- gi No. 1346526
- % Identity 90.6
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
  
- Alignment No. 8895
- gi No. 147855
- % Identity 71.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1013: from 7 to 52
  
- Alignment No. 8896
- gi No. 1708995
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8897
- gi No. 1709000
- % Identity 94.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
  
- Alignment No. 8898
- gi No. 1709001
- % Identity 85.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1013: from 30 to 95
  
- Alignment No. 8899
- gi No. 1709002
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8900
- gi No. 1709004
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8901
- gi No. 1709006
- % Identity 90.2
- Alignment Length 61
- Location of Alignment in SEQ ID NO 1013: from 36 to 95

- Alignment No. 8902
- gi No. 172534
- % Identity 70.2
- Alignment Length 94
- Location of Alignment in SEQ ID NO 1013: from 3 to 95
  
- Alignment No. 8903
- gi No. 2129889
- % Identity 90.6
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
  
- Alignment No. 8904
- gi No. 2315140
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8905
- gi No. 2665652
- % Identity 72.9
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
  
- Alignment No. 8906
- gi No. 3024121
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8907
- gi No. 3024122
- % Identity 95.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
  
- Alignment No. 8908
- gi No. 3024126
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8909
- gi No. 3024127
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8910
- gi No. 3024148
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8911
- gi No. 3914019
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8912

- gi No. 4883604
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8913
- gi No. 4894592
- % Identity 72.9
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
  
- Alignment No. 8914
- gi No. 4927188
- % Identity 71.9
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
  
- Alignment No. 8915
- gi No. 5726594
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
  
- Alignment No. 8916
- gi No. 609557
- % Identity 85.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1013: from 30 to 95

Maximum Length Sequence corresponding to clone ID 225478

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1014
- Ceres seq\_id 1499422

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1015
- Ceres seq\_id 1499423
- Location of start within SEQ ID NO 1014: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1016
- Ceres seq\_id 1499424
- Location of start within SEQ ID NO 1014: at 73 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8917
- 3' exoribonuclease family
- Location within SEQ ID NO 1016: from 40 to 134 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1017
- Ceres seq\_id 1499425
- Location of start within SEQ ID NO 1014: at 121 nt.



(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8918
- 3' exoribonuclease family
- Location within SEQ ID NO 1017: from 24 to 118 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 230791

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1018
- Ceres seq\_id 1499446

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1019
- Ceres seq\_id 1499447
- Location of start within SEQ ID NO 1018: at 111 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8919
- Mur ligase family
- Location within SEQ ID NO 1019: from 60 to 127 aa.
- Alignment No. 8920
- Mur ligase family
- Location within SEQ ID NO 1019: from 121 to 305 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8921
- gi No. 1706885
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1019: from 452 to 468
- Alignment No. 8922
- gi No. 2137297
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1019: from 452 to 468
- Alignment No. 8923
- gi No. 2137812
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1019: from 452 to 468

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1020
- Ceres seq\_id 1499448
- Location of start within SEQ ID NO 1018: at 282 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8924
- Mur ligase family
- Location within SEQ ID NO 1020: from 3 to 70 aa.
- Alignment No. 8925
- Mur ligase family
- Location within SEQ ID NO 1020: from 64 to 248 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8926
- gi No. 1706885
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1020: from 395 to 411
  
- Alignment No. 8927
- gi No. 2137297
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1020: from 395 to 411
  
- Alignment No. 8928
- gi No. 2137812
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1020: from 395 to 411

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1021
- Ceres seq\_id 1499449
- Location of start within SEQ ID NO 1018: at 612 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8929
- Mur ligase family
- Location within SEQ ID NO 1021: from 1 to 138 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8930
- gi No. 1706885
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1021: from 285 to 301
  
- Alignment No. 8931
- gi No. 2137297
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1021: from 285 to 301
  
- Alignment No. 8932
- gi No. 2137812
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1021: from 285 to 301

Maximum Length Sequence corresponding to clone ID 230831

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1022
- Ceres seq\_id 1499450

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1023
- Ceres seq\_id 1499451
- Location of start within SEQ ID NO 1022: at 501 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8933
- gi No. 4204290
- % Identity 82.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1023: from 282 to 356
  
- Alignment No. 8934
- gi No. 4204290
- % Identity 80.6
- Alignment Length 248
- Location of Alignment in SEQ ID NO 1023: from 3 to 250
  
- Alignment No. 8935
- gi No. 4322421
- % Identity 98.6
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1023: from 3 to 357
  
- Alignment No. 8936
- gi No. 4768281
- % Identity 99.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1023: from 3 to 357
  
- Alignment No. 8937
- gi No. 5305736
- % Identity 99.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1023: from 3 to 357

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1024
- Ceres seq\_id 1499452
- Location of start within SEQ ID NO 1022: at 552 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8938
- gi No. 4204290
- % Identity 82.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1024: from 265 to 339
  
- Alignment No. 8939
- gi No. 4204290
- % Identity 80.6
- Alignment Length 248
- Location of Alignment in SEQ ID NO 1024: from 1 to 233
  
- Alignment No. 8940
- gi No. 4322421
- % Identity 98.6
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1024: from 1 to 340
  
- Alignment No. 8941
- gi No. 4768281
- % Identity 99.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1024: from 1 to 340

- Alignment No. 8942
- gi No. 5305736
- % Identity 99.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1024: from 1 to 340

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1025
- Ceres seq\_id 1499453
- Location of start within SEQ ID NO 1022: at 639 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8943
- gi No. 4204290
- % Identity 82.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1025: from 236 to 310
  
- Alignment No. 8944
- gi No. 4204290
- % Identity 80.6
- Alignment Length 248
- Location of Alignment in SEQ ID NO 1025: from 1 to 204
  
- Alignment No. 8945
- gi No. 4322421
- % Identity 98.6
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1025: from 1 to 311
  
- Alignment No. 8946
- gi No. 4768281
- % Identity 99.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1025: from 1 to 311
  
- Alignment No. 8947
- gi No. 5305736
- % Identity 99.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1025: from 1 to 311

Maximum Length Sequence corresponding to clone ID 230894

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1026
- Ceres seq\_id 1499458

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1027
- Ceres seq\_id 1499459
- Location of start within SEQ ID NO 1026: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8948
- gi No. 2191127
- % Identity 99.4
- Alignment Length 177

- Location of Alignment in SEQ ID NO 1027: from 227 to 403
- Alignment No. 8949
- gi No. 3193306
- % Identity 97
- Alignment Length 201
- Location of Alignment in SEQ ID NO 1027: from 1 to 201

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1028
- Ceres seq\_id 1499460
- Location of start within SEQ ID NO 1026: at 55 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8950
- gi No. 2191127
- % Identity 99.4
- Alignment Length 177
- Location of Alignment in SEQ ID NO 1028: from 209 to 385
- Alignment No. 8951
- gi No. 3193306
- % Identity 97
- Alignment Length 201
- Location of Alignment in SEQ ID NO 1028: from 1 to 183

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1029
- Ceres seq\_id 1499461
- Location of start within SEQ ID NO 1026: at 85 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8952
- gi No. 2191127
- % Identity 99.4
- Alignment Length 177
- Location of Alignment in SEQ ID NO 1029: from 199 to 375
- Alignment No. 8953
- gi No. 3193306
- % Identity 97
- Alignment Length 201
- Location of Alignment in SEQ ID NO 1029: from 1 to 173

Maximum Length Sequence corresponding to clone ID 230897

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1030
- Ceres seq\_id 1499462

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1031
- Ceres seq\_id 1499463
- Location of start within SEQ ID NO 1030: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1032
- Ceres seq\_id 1499464
- Location of start within SEQ ID NO 1030: at 84 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8954
- gi No. 2651297
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1032: from 1 to 39

Maximum Length Sequence corresponding to clone ID 230925

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1033
- Ceres seq\_id 1499465

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1034
- Ceres seq\_id 1499466
- Location of start within SEQ ID NO 1033: at 105 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8955
- gi No. 3834313
- % Identity 99
- Alignment Length 195
- Location of Alignment in SEQ ID NO 1034: from 1 to 195

Maximum Length Sequence corresponding to clone ID 231096

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1035
- Ceres seq\_id 1499467

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1036
- Ceres seq\_id 1499468
- Location of start within SEQ ID NO 1035: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1037
- Ceres seq\_id 1499469
- Location of start within SEQ ID NO 1035: at 591 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8956
- gi No. 4835243
- % Identity 77.7
- Alignment Length 175
- Location of Alignment in SEQ ID NO 1037: from 1 to 119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1038

- Ceres seq\_id 1499470
- Location of start within SEQ ID NO 1035: at 651 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 8957
  - gi No. 4835243
  - % Identity 77.7
  - Alignment Length 175
  - Location of Alignment in SEQ ID NO 1038: from 1 to 99

Maximum Length Sequence corresponding to clone ID 231239

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1039
- Ceres seq\_id 1499474

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1040
- Ceres seq\_id 1499475
- Location of start within SEQ ID NO 1039: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1041
- Ceres seq\_id 1499476
- Location of start within SEQ ID NO 1039: at 573 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8958
- Syntaxin
- Location within SEQ ID NO 1041: from 1 to 140 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1042
- Ceres seq\_id 1499477
- Location of start within SEQ ID NO 1039: at 756 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8959
- Syntaxin
- Location within SEQ ID NO 1042: from 1 to 79 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 231303

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1043
- Ceres seq\_id 1499486

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1044
- Ceres seq\_id 1499487
- Location of start within SEQ ID NO 1043: at 84 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8960
- gi No. 2129778
- % Identity 70.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1044: from 22 to 85
  
- Alignment No. 8961
- gi No. 3236241
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1044: from 13 to 25
  
- Alignment No. 8962
- gi No. 4581965
- % Identity 70.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1044: from 22 to 85

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1045
- Ceres seq\_id 1499488
- Location of start within SEQ ID NO 1043: at 99 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8963
- gi No. 2129778
- % Identity 70.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1045: from 17 to 80
  
- Alignment No. 8964
- gi No. 3236241
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1045: from 8 to 20
  
- Alignment No. 8965
- gi No. 4581965
- % Identity 70.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1045: from 17 to 80

Maximum Length Sequence corresponding to clone ID 231598

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1046
- Ceres seq\_id 1499501

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1047
- Ceres seq\_id 1499502
- Location of start within SEQ ID NO 1046: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8966
- ParA family ATPase
- Location within SEQ ID NO 1047: from 278 to 364 aa.



(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1048
- Ceres seq\_id 1499503
- Location of start within SEQ ID NO 1046: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8967
- ParA family ATPase
- Location within SEQ ID NO 1048: from 262 to 348 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1049
- Ceres seq\_id 1499504
- Location of start within SEQ ID NO 1046: at 445 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8968
- ParA family ATPase
- Location within SEQ ID NO 1049: from 130 to 216 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 231731

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1050
- Ceres seq\_id 1499509

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1051
- Ceres seq\_id 1499510
- Location of start within SEQ ID NO 1050: at 52 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8969
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1051: from 92 to 159 aa.
- Alignment No. 8970
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1051: from 259 to 322 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1052
- Ceres seq\_id 1499511
- Location of start within SEQ ID NO 1050: at 55 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8971
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1052: from 91 to 158 aa.

- Alignment No. 8972
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1052: from 258 to 321 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1053
- Ceres seq\_id 1499512
- Location of start within SEQ ID NO 1050: at 535 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8973
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1053: from 98 to 161 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 231750

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1054
- Ceres seq\_id 1499513

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1055
- Ceres seq\_id 1499514
- Location of start within SEQ ID NO 1054: at 318 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8974
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1055: from 134 to 182 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8975
- gi No. 2244797
- % Identity 97.8
- Alignment Length 274
- Location of Alignment in SEQ ID NO 1055: from 12 to 283

Maximum Length Sequence corresponding to clone ID 231906

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1056
- Ceres seq\_id 1499519

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1057
- Ceres seq\_id 1499520
- Location of start within SEQ ID NO 1056: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8976
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1057: from 99 to 169 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1058
- Ceres seq\_id 1499521

- Location of start within SEQ ID NO 1056: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8977
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1058: from 76 to 146 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1059
- Ceres seq\_id 1499522
- Location of start within SEQ ID NO 1056: at 136 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8978
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1059: from 54 to 124 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 231948

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1060
- Ceres seq\_id 1499523

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1061
- Ceres seq\_id 1499524
- Location of start within SEQ ID NO 1060: at 187 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8979
- Zinc finger, CCHC class
- Location within SEQ ID NO 1061: from 196 to 213 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8980
- gi No. 2760333
- % Identity 99.7
- Alignment Length 287
- Location of Alignment in SEQ ID NO 1061: from 116 to 402

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1062
- Ceres seq\_id 1499525
- Location of start within SEQ ID NO 1060: at 244 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8981
- Zinc finger, CCHC class
- Location within SEQ ID NO 1062: from 177 to 194 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8982
- gi No. 2760333
- % Identity 99.7
- Alignment Length 287

- Location of Alignment in SEQ ID NO 1062: from 97 to 383

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1063
- Ceres seq\_id 1499526
- Location of start within SEQ ID NO 1060: at 256 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8983
- Zinc finger, CCHC class
- Location within SEQ ID NO 1063: from 173 to 190 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8984
- gi No. 2760333
- % Identity 99.7
- Alignment Length 287
- Location of Alignment in SEQ ID NO 1063: from 93 to 379

Maximum Length Sequence corresponding to clone ID 231976

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1064
- Ceres seq\_id 1499527

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1065
- Ceres seq\_id 1499528
- Location of start within SEQ ID NO 1064: at 107 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8985
- gi No. 4586255
- % Identity 90.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 1065: from 1 to 95
- Alignment No. 8986
- gi No. 4586255
- % Identity 79.3
- Alignment Length 213
- Location of Alignment in SEQ ID NO 1065: from 59 to 271

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1066
- Ceres seq\_id 1499529
- Location of start within SEQ ID NO 1064: at 203 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8987
- gi No. 4586255
- % Identity 90.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 1066: from 1 to 63
- Alignment No. 8988
- gi No. 4586255
- % Identity 79.3

- Alignment Length 213
- Location of Alignment in SEQ ID NO 1066: from 27 to 239

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1067
- Ceres seq\_id 1499530
- Location of start within SEQ ID NO 1064: at 257 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8989
- gi No. 4586255
- % Identity 90.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 1067: from 1 to 45
- Alignment No. 8990
- gi No. 4586255
- % Identity 79.3
- Alignment Length 213
- Location of Alignment in SEQ ID NO 1067: from 9 to 221

Maximum Length Sequence corresponding to clone ID 232208

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1068
- Ceres seq\_id 1499538

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1069
- Ceres seq\_id 1499539
- Location of start within SEQ ID NO 1068: at 172 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8991
- gi No. 1168470
- % Identity 72.5
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1069: from 1 to 90
- Alignment No. 8992
- gi No. 3461835
- % Identity 92.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1069: from 1 to 90

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1070
- Ceres seq\_id 1499540
- Location of start within SEQ ID NO 1068: at 241 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8993
- gi No. 1168470
- % Identity 72.5
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1070: from 1 to 67

- Alignment No. 8994
- gi No. 3461835
- % Identity 92.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1070: from 1 to 67

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1071
- Ceres seq\_id 1499541
- Location of start within SEQ ID NO 1068: at 257 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 232227

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1072
- Ceres seq\_id 1499542

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1073
- Ceres seq\_id 1499543
- Location of start within SEQ ID NO 1072: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8995
- gi No. 3776560
- % Identity 72.8
- Alignment Length 245
- Location of Alignment in SEQ ID NO 1073: from 190 to 432
  
- Alignment No. 8996
- gi No. 4587563
- % Identity 99.8
- Alignment Length 420
- Location of Alignment in SEQ ID NO 1073: from 14 to 433

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1074
- Ceres seq\_id 1499544
- Location of start within SEQ ID NO 1072: at 40 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8997
- gi No. 3776560
- % Identity 72.8
- Alignment Length 245
- Location of Alignment in SEQ ID NO 1074: from 177 to 419
  
- Alignment No. 8998
- gi No. 4587563
- % Identity 99.8
- Alignment Length 420
- Location of Alignment in SEQ ID NO 1074: from 1 to 420

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1075

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- Ceres seq\_id 1499545
- Location of start within SEQ ID NO 1072: at 397 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8999
- gi No. 3776560
- % Identity 72.8
- Alignment Length 245
- Location of Alignment in SEQ ID NO 1075: from 58 to 300
  
- Alignment No. 9000
- gi No. 4587563
- % Identity 99.8
- Alignment Length 420
- Location of Alignment in SEQ ID NO 1075: from 1 to 301

Maximum Length Sequence corresponding to clone ID 232986

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1076
- Ceres seq\_id 1499547

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1077
- Ceres seq\_id 1499548
- Location of start within SEQ ID NO 1076: at 220 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9001
- gi No. 1076641
- % Identity 72.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1077: from 1 to 101
  
- Alignment No. 9002
- gi No. 1170711
- % Identity 71.6
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1077: from 1 to 101
  
- Alignment No. 9003
- gi No. 1431622
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1077: from 68 to 101
  
- Alignment No. 9004
- gi No. 1480078
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1077: from 32 to 101
  
- Alignment No. 9005
- gi No. 1709129
- % Identity 75
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1077: from 1 to 101
  
- Alignment No. 9006

- gi No. 2129738
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1077: from 33 to 101
  
- Alignment No. 9007
- gi No. 2129739
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1077: from 35 to 101
  
- Alignment No. 9008
- gi No. 2182029
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 1077: from 42 to 101
  
- Alignment No. 9009
- gi No. 2398519
- % Identity 71.6
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1077: from 1 to 101
  
- Alignment No. 9010
- gi No. 3201623
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1077: from 33 to 101
  
- Alignment No. 9011
- gi No. 4539390
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1077: from 35 to 101

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1078
- Ceres seq\_id 1499549
- Location of start within SEQ ID NO 1076: at 301 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9012
- gi No. 1076641
- % Identity 72.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1078: from 1 to 74
  
- Alignment No. 9013
- gi No. 1170711
- % Identity 71.6
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1078: from 1 to 74
  
- Alignment No. 9014
- gi No. 1431622
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1078: from 41 to 74



- Alignment No. 9015
- gi No. 1480078
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1078: from 5 to 74
  
- Alignment No. 9016
- gi No. 1709129
- % Identity 75
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1078: from 1 to 74
  
- Alignment No. 9017
- gi No. 2129738
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1078: from 6 to 74
  
- Alignment No. 9018
- gi No. 2129739
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1078: from 8 to 74
  
- Alignment No. 9019
- gi No. 2182029
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 1078: from 15 to 74
  
- Alignment No. 9020
- gi No. 2398519
- % Identity 71.6
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1078: from 1 to 74
  
- Alignment No. 9021
- gi No. 3201623
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1078: from 6 to 74
  
- Alignment No. 9022
- gi No. 4539390
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1078: from 8 to 74

Maximum Length Sequence corresponding to clone ID 246205

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1079
- Ceres seq\_id 1499558

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1080
- Ceres seq\_id 1499559
- Location of start within SEQ ID NO 1079: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 9023

- gi No. 1172663
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1080: from 100 to 122
  
- Alignment No. 9024
- gi No. 131185
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1080: from 101 to 119
  
- Alignment No. 9025
- gi No. 131186
- % Identity 88.9
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1080: from 101 to 118
  
- Alignment No. 9026
- gi No. 3885892
- % Identity 73.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1080: from 27 to 131
  
- Alignment No. 9027
- gi No. 478522
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1080: from 100 to 123
  
- Alignment No. 9028
- gi No. 548604
- % Identity 73.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1080: from 27 to 131

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1081
- Ceres seq\_id 1499560
- Location of start within SEQ ID NO 1079: at 81 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9029
- gi No. 1172663
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1081: from 74 to 96
  
- Alignment No. 9030
- gi No. 131185
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1081: from 75 to 93
  
- Alignment No. 9031
- gi No. 131186
- % Identity 88.9
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1081: from 75 to 92

- Alignment No. 9032
- gi No. 3885892
- % Identity 73.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1081: from 1 to 105
  
- Alignment No. 9033
- gi No. 478522
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1081: from 74 to 97
  
- Alignment No. 9034
- gi No. 548604
- % Identity 73.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1081: from 1 to 105

Maximum Length Sequence corresponding to clone ID 246509

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1082
- Ceres seq\_id 1499567

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1083
- Ceres seq\_id 1499568
- Location of start within SEQ ID NO 1082: at 111 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9035
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1083: from 11 to 78 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9036
- gi No. 3386565
- % Identity 95
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1083: from 1 to 78

Maximum Length Sequence corresponding to clone ID 246543

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1084
- Ceres seq\_id 1499576

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1085
- Ceres seq\_id 1499577
- Location of start within SEQ ID NO 1084: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9037
- gi No. 100448
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9038
- gi No. 100449
- % Identity 76.9

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- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9039
- gi No. 1076665
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9040
- gi No. 1086103
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9041
- gi No. 129640
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9042
- gi No. 129641
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9043
- gi No. 129642
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9044
- gi No. 129643
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9045
- gi No. 129644
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9046
- gi No. 169497
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1085: from 27 to 46
  
- Alignment No. 9047
- gi No. 169520
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
  
- Alignment No. 9048
- gi No. 21415
- % Identity 76.9
- Alignment Length 26

- Location of Alignment in SEQ ID NO 1085: from 27 to 52
- Alignment No. 9049
- gi No. 261222
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
- Alignment No. 9050
- gi No. 320598
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
- Alignment No. 9051
- gi No. 695756
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
- Alignment No. 9052
- gi No. 82272
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1086
- Ceres seq\_id 1499578
- Location of start within SEQ ID NO 1084: at 22 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9053
- gi No. 100448
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9054
- gi No. 100449
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9055
- gi No. 1076665
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9056
- gi No. 1086103
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9057
- gi No. 129640
- % Identity 76.9

- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9058
- gi No. 129641
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9059
- gi No. 129642
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9060
- gi No. 129643
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9061
- gi No. 129644
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9062
- gi No. 169497
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1086: from 20 to 39
- Alignment No. 9063
- gi No. 169520
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9064
- gi No. 21415
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9065
- gi No. 261222
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9066
- gi No. 320598
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9067
- gi No. 695756
- % Identity 76.9
- Alignment Length 26

- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9068
- gi No. 82272
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1087
- Ceres seq\_id 1499579
- Location of start within SEQ ID NO 1084: at 104 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 246728

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1088
- Ceres seq\_id 1499591

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1089
- Ceres seq\_id 1499592
- Location of start within SEQ ID NO 1088: at 94 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9069
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1089: from 43 to 127 aa.

- Alignment No. 9070
- Adhesion lipoprotein
- Location within SEQ ID NO 1089: from 24 to 113 aa.

- Alignment No. 9071
- Adhesion lipoprotein
- Location within SEQ ID NO 1089: from 74 to 125 aa.

- Alignment No. 9072
- Osteopontin
- Location within SEQ ID NO 1089: from 6 to 124 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9073
- gi No. 2209095
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1089: from 106 to 123

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1090
- Ceres seq\_id 1499593
- Location of start within SEQ ID NO 1088: at 187 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9074
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1090: from 12 to 96 aa.

- Alignment No. 9075
- Adhesion lipoprotein
- Location within SEQ ID NO 1090: from 1 to 82 aa.
  
- Alignment No. 9076
- Adhesion lipoprotein
- Location within SEQ ID NO 1090: from 43 to 94 aa.
  
- Alignment No. 9077
- Osteopontin
- Location within SEQ ID NO 1090: from 1 to 93 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9078
- gi No. 2209095
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1090: from 75 to 92

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1091
- Ceres seq\_id 1499594
- Location of start within SEQ ID NO 1088: at 214 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9079
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1091: from 3 to 87 aa.
  
- Alignment No. 9080
- Adhesion lipoprotein
- Location within SEQ ID NO 1091: from 1 to 73 aa.
  
- Alignment No. 9081
- Adhesion lipoprotein
- Location within SEQ ID NO 1091: from 34 to 85 aa.
  
- Alignment No. 9082
- Osteopontin
- Location within SEQ ID NO 1091: from 1 to 84 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9083
- gi No. 2209095
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1091: from 66 to 83

Maximum Length Sequence corresponding to clone ID 246776

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1092
- Ceres seq\_id 1499605

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1093
- Ceres seq\_id 1499606
- Location of start within SEQ ID NO 1092: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)



(D) Related Amino Acid Sequences

- Alignment No. 9084
- gi No. 1172977
- % Identity 88.5
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1093: from 23 to 48
  
- Alignment No. 9085
- gi No. 2501187
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1093: from 48 to 84
  
- Alignment No. 9086
- gi No. 2501188
- % Identity 91.9
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1093: from 48 to 84
  
- Alignment No. 9087
- gi No. 2501189
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1093: from 48 to 84
  
- Alignment No. 9088
- gi No. 2529670
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1093: from 24 to 48
  
- Alignment No. 9089
- gi No. 2582665
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1093: from 48 to 86
  
- Alignment No. 9090
- gi No. 3021348
- % Identity 78.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1093: from 26 to 48
  
- Alignment No. 9091
- gi No. 3650384
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1093: from 50 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1094
- Ceres seq\_id 1499607
- Location of start within SEQ ID NO 1092: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9092
- gi No. 1172977
- % Identity 88.5
- Alignment Length 26

- Location of Alignment in SEQ ID NO 1094: from 1 to 26
- Alignment No. 9093
- gi No. 2501187
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1094: from 26 to 62
- Alignment No. 9094
- gi No. 2501188
- % Identity 91.9
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1094: from 26 to 62
- Alignment No. 9095
- gi No. 2501189
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1094: from 26 to 62
- Alignment No. 9096
- gi No. 2529670
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1094: from 2 to 26
- Alignment No. 9097
- gi No. 2582665
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1094: from 26 to 64
- Alignment No. 9098
- gi No. 3021348
- % Identity 78.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1094: from 4 to 26
- Alignment No. 9099
- gi No. 3650384
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1094: from 28 to 59

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1095
- Ceres seq\_id 1499608
- Location of start within SEQ ID NO 1092: at 152 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9100
- gi No. 2501187
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1095: from 1 to 34
- Alignment No. 9101
- gi No. 2501188
- % Identity 91.9